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Listing first 45 summaries
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897
2888711 seqs, 20454813386 residues
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Pred. No. is the number of results predicted by chance to have a

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AUTHORS	KEYWORDS SOURCE ORGANISM	RESULT 1 AX134720 LOCUS DEFINITION ACCESSION VERSION		44	ωΝ	41	000	37	თ თ		w KO	Р С	900	ю ч	o 0	1 42- (ມເ		ο ω	8 7	100	J1 +₽	ωκ	3 12	01						-	Result No.	
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interaction	Vertebrata; ; Hominidae;	linear		AX134 AX301	AC111 AC110	AC135	AC130	BC008	AF231 BC043	X745	U273	BC00	BC00	0104	AB065	AX301	D127	AX401 D127	AB088	AB009	AF506	AC125	J0359	AX337	M2410	BC014	BC007	BC007	BC008	AX301	AX134	Desci	
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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through the I.M.A.G.B. Consortium/LLNL at: http://im
Series: IRAK Plate: 42 ROW: p Column: 5
This clone was selected for full length sequencing b
passed the following selection criteria: Similarity
                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., García, A.M., Lu, X., Huly.
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
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Submitted (06-JUN-2002) National Institutes of Headene Collection (MGC), Cancer Genomics Office, National Institute, 31 Center Drive, Room 11A03, Bethesda,
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Tissue Procurement: ATCC
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Contact: MGC help desk
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              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="LocusID: 293"
/db_xref="taxon: 9606"
/clone="MGC: 29984 INAGE: 5141625"
/tissue_type="Cervix, carcinoma"
/clone_lib="NIH_MGC_12"
                                                                                                                                           to protein.
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/protein_id="AAH31912.1"
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/db_xref="GI:21594693"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
Contact: amadan/systemsbiology.org
Contact: Amadan/syst
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 9956
Location/Qualifiers
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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Tissue Procurement: DCTD/DTP
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Submitted (29-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                   /translation="MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
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LVKITKSDGIRGLYQGFSVSVQGIIIYRAAYEGVYDTAKGHLDDRKNTHIVSWMIAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pOTB7"
94. .990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"

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/db_xref="taxon:9606"

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/clone_lib="NIH_MGC.7"

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                                                                                                                                                                                                                                                                                                                                                                       member 5"
                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                            NVLRGMGGAFVLVLYDELKKVI'
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/db_xref="GI:14286274"
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                                                                                                                  a
Score 895.4;
Pred. No. 1.1
                                                                                                                  355
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   .4; DB 9;
1.1e-131;
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                                ACCESSION
VERSION
KEYWORDS
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BC007295
LOCUS
DEFINITION
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                                                                                    Homo sapiens solute carrier family 25 (mi adenine nucleotide translocator), member WGC:15671 IMAGE:3349670), complete cds. BC007295
                                                                 BC007295.1 GI:13938330
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                                                                                                                                                  6, mRNA (cDNA clone
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813

693 600 633 540 573 480 513 453

393

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PUBMED
REFERENCE
AUTHORS
TITLE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J. W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Haiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 22 Row: m Column: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC Cancer Agency, Vancouver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      info@bcgsc.bc.ca
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Library Arrayed by: The I.M.A.G.E. Consortium
Sequencing by: Genome Sequence Centre,
ancer Agency, Vancouver, BC, Canada
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       /product="solute carrier family 25, member A6"
                                                                                                                                                                                     /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                     /db_xref="MIM:403000"
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GGCATGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCCC
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                                                                                          ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG
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780 772 660

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420 412 360 352 300 292 240 232

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NVLRGMGGAFVLVLYDELKKVI
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Score 895.4; Pred. No. 1.1 DB Length 1308;

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Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The clone request should be directed to Dr. J. Margolin at Pediatrics-Hematology & Oncology, Texas Children's FEIGIN Center 102514, Houston, Texas 77030, USA. Telephone: 713-770-4583 margolin@bcm.tmc.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W., Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A. Large-scale concatenation cDNA sequencing Genome Res. 7 (4), 353-358 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu, W., Anderson
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1 (bases 1 to 1344)

1 Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A. A 'double adaptor' method for improved shotgun library construction anal. Biochem. 236 (1), 107-113 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC 120
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90. 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1"
                                                                                                                                                                                                                                                                                                                                                                                   NVLRGMGGAFVLVLYDELKKVI"
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                                                                                                                                                                                                        Score 895.4; DB 9;
pred. No. 1.1e-131;
0; Mismatches 1;
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330 TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
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Direct Submission
Submitted (11-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                           BC007850 1366 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, clone MGC:14294 IMAGE:4136545, mRNA, complete cds.
                                                                                             Strausberg, R.
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1366)
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                                                                                                                                                                                                                                Homo sapiens (human)
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through
Series:
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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through the I.M.A.G.E. Consortium/LLNL at: http://image.lln
Series: IRAL Plate: 20 Row: 1 Column: 14
This clone was selected for full length sequencing because
passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                               ATCCCCAAGGAGCAGGGCTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC
                                                                                                                                   GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC
                                                                                                                                                              GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC
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cgapbs-r@mail.nih.gov
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/PIOTELIN_1d-"AAH07850.1"
/PIOTELIN_1d-"AFA03791"
/TIANSLATION-"MTEQALSFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
/TANSLATION-"MTEQALSFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
IAADKQYKGIVDCIVALPKEGGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGG
VDKHTQFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGIGDC
LYKITKSDGIRGLYQGFSVSVQGIIIYKAAYFGVYDTAKGMLPDPKNTHIVVSNMIAQ
TVTAVAGGVSVFPDTVRRRMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWS
NVLRGMGGAFVLVLYDELKKVI"
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/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MCC), Cancer Genomics Office, National Cancer Gene Collection (MCC), Cancer Genomics Office, National Cancer Gene Collection (MCC), Cancer Genomics Office, National Cancer General National Cancer C
                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortiu DNA Sequencing by: Baylor College of Medicine Hum
                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                        NIH-MGC Project URL: http://mgc
Contact: MGC help desk
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Mammalia; 1
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mmalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 1455)
Sequencing by:
uencing Center
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                                                   Consortium (LLNL)
                           Human
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(mitochondrial
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453 GGTGCGGCCGGCGCGACCTCCCTCTGCTTCGTTACCCGCTGGATTTTGCCAGAACCCGC
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalonebcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., CVIllalon, D.K., Luna, R.A., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plates: 19 Row: p Column: 11.
Location/Qualifiers
                                            CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC 540
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/clone="MGC:17525 INAGE:3458777"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAH14775.1"
//Ab_xref="GI:19928608"
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//EI anslation="MTEDAISFERDFLAGGIAAAISKTAVAPIERVKLLLOVOHASKO
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TYTAVAGVVSYPEDTYFRRHMMOPGRKGADIMYTGTYDCWRKIFRDEGGKAFFKGAWS
NVLRGMGGAFYLVLYDELKKVI"
a
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/product="Similar to solute carrier family 25
(mitochondrial carrier; adenine nucleotide translocator),
member 5
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Pred. No. 1.1e-131;
0; Mismatches 1;
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/ILML at: http://image.llnl.gov Series: IRAL Plate: 5 Row: o Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF

information can be found

REMARK COMMENT	RESULT 9 BCOOR737 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION RETWORDS SOURCE ORGANISM REFERENCE ACTHORS JOURNAL	D Q D Q D D Q D D D D D D D D D D D D D	
NIH-MGC Project URL: http://mgc.nci.nih.gov NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: ogapbs-remail.nih.gov Tissue procurement: ATCC CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: nisc_mgcenhgri.nih.gov/ Contact: nisc_mgcenhgri.nih.gov Shevchenko, Y. Wetherby K.D. Beckstrom-Sternberg, S.M., Shevchenko, Y. Wetherby K.D. Beckstrom-Sternberg, S.M., Benjamin, B. Blakesley, R.W. Bouffard, G.G., Brinkiey, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, SL., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantipop, S., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, LH. and Green, E.D.	OS STANDER HOO BOOK BOOK BOOK BOOK BOOK BOOK BOOK	573 CTGGTGAAGATCAACATCTAACGAGGCCTACCTTCGGGGCCTTAACGAGGCCTTCAGTTCTACCAAGGCCTAACGAGTCTCGGGGCCTTCAGTTACCAAGGCCTAACGAGGCCTAACTTCGGGGCCTTCAGTTACCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGACACACCAC	

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                    ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POWEIL,S.J., Medd,S.M., Runswick,M.J. and W
Two bovine genes for mitochondrial ADP/ATP
differences in various tissues
Biochemistry 28 (2), 866-873 (1989)
R9220003
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                  Similarity
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                                                                                                                       ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGAGGCAGCGCCGCCGCC
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                                            ATCTCCAAGACTGCCGTTGCCCCGATCGAGCGCGTCAAGCTCCTGCTGCAGGTGCAGCAC
                                                                                                       ATGACGGAACAGGCCATCTCCCTTCGCCAAGGATTTCCTGGCCGGGGGGCATCGCCGCCCC
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                                                                                                                                                                                                                                                                      /product="translocase"
/protein_id="AAA30769.1"
/protein_id="AAA30769.1"
/db_xref="Gi: 529417"
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/translation="MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
/translation="MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQ
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/TVTAVAGVVSYPEDTVRRMMAGSGRKGADIMYKGTVDCWRKILKDEGGKAFFKGAWS
                                                                                                                                                                                                                                             NVLRGMGGAFVLVLYDELKKVI"
447 c 409 g 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
/mol_type="mRNA"
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0; Mismatches
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actyla; Ruminantia; Pecora;
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1.3e-112;
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                                                                                                  Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
                                                             Avalon
                                                                                         gene sets
                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
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Sequence 7684 from Patent WO0194629,
AX337175
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                         AX337175.1 GI:18127894
                                                                                                                                                                                                                                                                                                                                                        GGCATGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGACGTCAAGAAGGTGATCTA 896
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                                                             Pharmaceuticals
                                                                         WO 0194629-A 7684 13-DEC-2001;
/organism="Homo sapiens"
/mol_type="genomic DNA"
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1. .1116
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                         AX409449 1116 bp I
Sequence 2096 from Patent WO0229103
AX409449 AX409449.1 GT:21442154
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Homo sapiens (human)
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Similarity 99.2%;
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Patent: WO 0229103-A 2096 11-APR-2002;
GENE LOGIC INC (US)
}
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  GACTGTTGGAGGAGATCTTCAGAGAGATGAGGGGGCAAGGCCTTCTTCAAGGGTGCGTGG
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  GACTGTTGGAGGAAGATCTTCAGAGATGAGGGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGG
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                           TCCAACGTCCTGCGGGGCATGGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/db_xref="EMBL/GenBank Accession
/note="EMBL/GenBank Accession
330 c 346 g 209 t
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Original source text:
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            TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA 465
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TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA
                                                    AACCTGGCCTCCGGCGGTGCGGCCGGCGCGACCTCCCTCTGCTTCGTGTACCCCGCTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA36750.1"
/db_xref="GI:339723"
/db_xref="GI:339723"
/db_xref="GI:339723"
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RYFPTQALNFAFKDKYKQIFLGGVDRHAFWRYFAGNLASGGAAGATSLCFVYPLDFAR
RYFPTQALNFAFKDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGYYD
TAKAALPDFKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRMMQSGRKGADIMYTGT
VDCWRKIFRDEGGKAFFKGAWSNVLRGMGAFYLVLYDELKKVI"
a 330 c 346 g 209 t
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/db_xref="+-
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99.2%;
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0; Mismatches 3;
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Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angulano,D.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angulano,D.,
Anyalabechi, V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranalke,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chen,C., Cockeell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Cleveland,C., Cockeell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Davis,C.A., Evens,C.A., Falls,T., Fan,G.,
Fanson,S., Deramo,C., Drobes,L., Foster,M., Foster,F.,
Fraser,C.M., Gablai,A., Ganta,R., Garcia,M., Guerra,W., Guerra,W., Gablai,A., Ganta,R., Garcia,M., Guerra,W., Guerra,W., Galli,R., Grady,M., Guerra,W., Guerra,W.,
Guaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Hernandez,R., Hines,S., Hadun,S.L., Hodgson,A., Hogues,M.,
Hernandez,R., Hines,S., Hlayk,S., Hume,J., Idlebird,D., Jackson,A.,
Karpathy,S., Keily,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Lil,Z., Liu,J.,
Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lu,W., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 ATCGCGCAGACCGTGACGGCCGTGGCCGGCGTGCTCCTACCCCTTCGACACGGTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

Rattus norvegicus (Norway rat)

Rattus norvegicus (Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC125887
AC125887.3 GI:25008671
HTG; HTGS_PHASE1; HTGS_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC125887 291762 bp DNA linear HTG 15-MOV-2002
Rattus norvegicus clone CH230-274J3, *** SEQUENCING IN PROGRESS
***, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTGTTGGAGGAAGATCTTCAGAGATGAGGGGGGGAAGGCCTTCTTCAAGGGTGCGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACTGTTGGAGGAAGATCTTCAGAGATGAGGGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGG
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Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M. P., McNeill, T.Z., Menenn, E., Milosavijevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Montemayor, J., Moore, S., Morgan, M., Morris, S., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nankervis, C., Newton, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Pepez, N., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Poloper, F., Poindexter, A., Popovic, D., Primus, E., Pul, T., Puzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Niegs, F., Kives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shyartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shety, J., Shartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shety, J., Shartsbeyn, A., Stason, I., Sitter, C.D., Smajs, D., Shedia, M., Strong, R., Sutton, A., Swatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, R., Welfar, M., Waller, M., Warren, R., Welfar, M., Waller, 
Direct Submission

Libratts Submission

Libratts Submission

Libratts Submission

Submitted (15-NOV-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23269681.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.higsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table sequences and whole genome table sequences and whole genome table sequences.
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Direct Submission
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

JOURNAL

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

---- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: ngsc-help@bcm.tmc.edu
Center project name: GMLD
Center clone name: CH230-274J3
Center clone name: CH230-274J3
Assembly program: Phrap; version 0.990329
Consensus quality: 236053 bases at least Q30
Consensus quality: 236053 bases at least Q30
Consensus quality: 230853 bases at least Q30
Consensus quality: 236053 bases at least Q30
Consensus quality: 230853 bases at least Q30
Consensu Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.lgsc.bcm.tmc.edu/docs/senbank_draft_data.html).

* NOTE: This is a "vorking draft" sequence. It currently

* consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

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FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
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Best Local
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                                                                                     32024
                                                                                                                                               32084
                                                                                                                                                                             181
                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                              61 ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC
                                                                                                                                                                                                                                                                                                                                                      1 ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                        GGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC
                                                                                    GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This record will as soon as it is be preserved.
 GGTGCGGCCGGCGCGCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC
                                            GGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCCAACCTTGGCCTCCGGC
                                                                                                               TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
                                                                                                                                                                         ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC
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109057. .110574
/note="wgs_contig"
a 50792 c 50314 g
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/clone="CH230-274J3"
70378. .75596
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/mol_type="genomic DNA"
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271197: gap of u
273126: gap of u
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of 4428
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of 13825 bp in
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                    where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31784
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                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mappi Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RPII-57/H4 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
AL354854
                                                                                                                                                                                                                               SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced g1:14625557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                             http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                              601 ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG 660
                                         103872 CAGTCCCGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 103931
                                                                                                                                                                                                                                                                         103632 CTAGTGAAGATCAGCAAGTCCGACGCATCCGGGGCCTTTACCAGGGCTTCAGCGTCTCC 103691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103410 TACTCCCCAAGCCCTCAATTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG 103469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103572 CTGGCAGCCGACGTGGGAAAGTCAGGCACGGAGCGCGAGTTCCGAGGCCTGGGAGACTGC 103631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103230 ATCTCCAAGACAGCCGTGGCATCGATCAAGCGGGTCCAGCTGCTGCTGCAGATGCAGCAC 103289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
                                                           721 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780
                                                                                                                                         421 CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAAACTGC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ATCCCCAAGGAGCAGGGCTGCTGCTGCTGGAGGGGCAACCTTGCCCAACGTCATTCGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC 360
                                                                                                                                                                                                                                                                                                                                                                                                   481 CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCCTTCAGTGTCTCC 540
  781 ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATCTCCAAGACGGCCGTGCCATCCGATCGAGCGGGTCAAGCTGCTGCTGCTGCAGGTCCAGCAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        left end of clone RP11-27103 is at 128593 in this sequence. The true right end of clone RP11-69L15 is at 36723 in this sequence rocation/Qualifiers
                                                                                                                    ACGGCCGTGGCTGCTCTCCTAACCCTTCGACACAGTGCGGCGGCGGACGATGATG 103871
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/mol_type="genomic DNA"

/db_xref="texon 9606"

/chromosome="9" 90606"

/clone="mp11-57244"

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/lone_tib="Republic Trom overlapping clone RP11-27103

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Search completed: August 24, 2003, 04:35:27 Job time: 3697 secs

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318.6	322.6	•	•	338.8	344.6	344.6	354.4	354.4	363	394	394	400.8	406.6	462.6	482.4	482.4	•	519.2	•		•	•	•	564:2	•	568.4		•	•			•	•		771.2	
35.5	36.0	36.3	37.0	37.8	38.4	38.4	39.5	39.5	40.5	43.9		44.7		٠			•	•	•	•		•	•	62.9		•	•	٠	•	•	•	•	•	•	•	
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ABX47259	AAX39617	ABL61797	ABN74435	ABT09322	ABL20966	ABL18530	ABX71399	AAD33664	AAS68190	ABS76969	ABS76857	AAS79610	ABN74319	ABL03127	ABK84798	AAS35083	AAS29836	ABL20967	ABL18531	ABZ33737	ABS65029	ABZ83302	AAS16688	AAS05901	AAD00519	AAS91243	AAV36479	AAV36480	AAS16689	AAS05902	AAD00520	AAL48635	ABK63420	ABQ56282	ABL69347	ABN95598
	Breast cancer asso		Bovine embryonic g	Phase-1 Rat CT gen	Drosophila melanog	Drosophila melanog		Human TRICH-19 cDN	(D)	embryonic	Frog embryonic gen	DNA encoding novel	Bovine embryonic g	Drosophila melanog	Human cDNA differe	DNA #33 encoding h	Human cytoskeletal	Drosophila melanog	Drosophila melanog	Human TRICH encodi	Invertebrate foraq	Toxicologically re	DNA encoding human	Human adenine nucl	Human adenine nucl	encoding	CDNA.	Antl cDNA. Mus sp	ncoding	adenine	adenine		Rat sequence diffe	3	tate cancer	Gene #2096 used to

ALIGNMENTS

29-AUG-2000 AAD00521; AAD00521 standard; (first entry) CDNA; 897 ВP

Human adenine nucleotide translocator ANT3 cDNA

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KW MI Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; disease; Parkinson's disease; Huntington's disease; dystonia; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome; ss. Homo sapiens. Location/Qualifiers
1..897 /product= "ANT3" /*tag=

WO200026370-A2.

11-MAY-2000.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, caber's hereditary optic neuropathy, schizophrenia, mitochondrial diabetes and deafness (MIDD), and myoclonic disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic capilepsy red ragged fibre syndrome. The present sequence is a cDNA cenceding adenine nucleotide translocator ANT3 from human brain.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other;
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DB; AAY71033.
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   CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAACTGC
                                      GGTGCGGCCGGCCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC 420
                                                                        TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
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                          GGTGCGGCCGCGCGACCTCCCTCTGCTTCGTGTACCCCGCTGGATTTTGCCAGAACCCGC
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                                                                                                                            TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
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99US-0393441.
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                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                  WPI; 2001-291054/30
P-PSDB; AAU01200.
                                                                                                                            (MITO-) MITOKOR.
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Human adenine nucleotide translocator-3 (ANT-3) cDNA sequence

Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss

Andreyev ΑY, Frigeri LG;

New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide

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Matches 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
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                         ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
                                                                                                                   CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCCTTCAGTGTCTCC
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Pred. No. 1.3e-175;
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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell an culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating
                                                                                                                                                                                                                                                       Novel
                                                                                                                                                                                                                           translocator nucleic acid
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                                                                                                                                                                                                                       recombinant expression construct locator polypeptides, comprises a sic acid encoding the polypeptide
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Y, Carroll !
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The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide CC of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system disease, smyotrophic CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic cand thrombolytic activity, arthritis and inflammation, leukaemias and CC Note: The sequence data for this patent did not form part of the printed corectification.
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                        C.N.S
                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzheiner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity-prager Syndrome. Other uses include the ActivinyInhibin activity, chemotactic/chemokinetic activity, damostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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Note: The sequence specification.
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                    (BAND/) BANDMAN O.
                                                        28-JUL-2000; 2000US-222469P
08-JAN-2001; 2001US-260483P
                                                                                                                 08-JAN-2002; 2002US-0044090
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CC are differentially expressed in activated vascular tissue. The invention calso discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have expressed cDNAs in a sample. The cDNAs of the invention may have called in gene therapy. The cDNAs of the invention may have used in gene therapy. The cDNAs of the invention may be used in gene therapy. The cDNAs of the invention may be used in a sample, or screening several molecules or compounds to high-throughput methods for detecting differential expression of one or compounds in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the convention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or crecombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, or monitoring the progression of creptination injury, restenosis, or stroke. The cDNAs can also be used conclete acid molecules. Antibodies to the proteins encoded by the cDNAs can also be used collaborated vascular disease, apre-echangeia, ischaemia-conclete acid molecules. Antibodies to the protests, and chronic consum to distribution of the protein. The present sequence creptesents a cDNA of the invention that is differentially expressed in contributed vascular tissue. Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated activated vascular tissue.

Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly frat http.seqdata.uspto.gov/sequence.html?DocID=20020137081. Claim 1; Page -; 18pp; English. comprises several vascular tissue -WPI; 2003-110597/10. Sequence 2592 BP; 520 A; 790 C; 766 G; 514 T; 2 other; ó from USPTO

207 896; Conservative 97.48; 0; Score 873.4; DB 25; Pred. No. 1e-170; 0; Mismatches 1;

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Liu TF,
Lewis SA,
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Nguyen
SA, Chen
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O, Yap PE, Amshey SR;
DA, Kleefeld Y, Gerstin
AJ, Panzer SR, Harris B;
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identifying test encoded by human human diagnostic and therapeutic polypeptide useful for ifying test compound which specifically binds to a polyped by human diagnostic and therapeutic polynucleotide, a antibodies y binds to a polypeptide polynucleotide, and to

Claim SEQ ID No 573; 591pp; English.

The invention relates to novel human diagnostic and therapeutic complynucleotides designated dithp (ACC46080-ACC46749) and to their concoded proteins (DITHP; ABR41138-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp CDNA compounds of the invention; recombinant vectors, host cells and concombinant production of DITHP proteins; antibodies specific for DITHP proteins; antibodies specific for DITHP proteins; antibodies specific for DITHP proteins and DITHP protein sequences; methods of compounds which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein; and methods of conditions including cancer and other cell proble. Dithp nucleic acid sequences and DITHP proteins may be used in the conditions including cancer and other cell conditions including cancer and other cell conditions including cancer and other cell conditions including cancers; metabolic conditions including cancers; metab ftp.wipo.int/pub/published_pct_sequences.

Sequence 2213 BP; 422 A; 751 Ç 633 <u>.</u> 407 T; 0 other;

δÃ 밁 δÃ 밁 Š 밁 δÃ 망 Ş 밁 Query Match Best Local S Matches 446 386 181 121 266 206 817; 61 Similarity TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC ATCCCCAAGGAGCAGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC Conservative 91.0%; 0; Score 816.4; Pred. No. 5.6e 0; Mismatches 816.4; DB 25 No. 5.6e-159; 25; Indels Length 2213; 0 Gaps 240 385 180 325 120 265

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RESULT 1

ABK83761

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KW Fung

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                                                                 Beazer-Barclay Y, Weissman
                                                                                                                                                   03-OCT-2000;
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity -Claim 1; SEQ ID No 332; 114pp; English.

The invention relates to detecting (MI) granulocyte (GC) activation (C (GCA), by detecting the level of expression of gene(s) (Gs) identified by CDNA (chip analysis as given in the specification, and comparing CC GC, where differential expression level in an unactivated CC GC, where differential expression of GS is indicative of GCA. CC Also included are modulating (M2) GA by contacting GC with an agent CC that alters the expression of at least one gene in Gs; (2) screening (M3) GC Aron an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a Subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression in a sample of the tissue of gene(s) from Gs, where CC the level of expression in a sample of the tissue of judicative of inflammation (especially CC chronic) in a tissue, an inflammation (especially CC chronic) in a tissue, an altergic response in a subject to a pathogen or sterile inflammatory disease, by detecting the CC an altergic response in a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an inflammation (especially chronic) or in a tissue, and inflammation (especially chronic) in a tissue, an altergic response in a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having sustful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile conflammation (especially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile conflammatory disease, crohirs d Sequence ftp.wipo.int/pub/published_pct_sequences. 1116 BP; 231 A; 330 C; 346 G; 209 T; 0 other;

Query Match Best Local Sim Matches 786; Similarity 86.0%; Score 771.2; DB 24; Length Pred. No. 1e-149; O; Mismatches 3; Indels

밁 Qy Ş 밁 5 밁 B 406 181 166 106 61 GCCAACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTAC CTGCAGGTCCAGCACGCCAGCAAGCAGATCGCCGCCACAAGCAGTACAAGGGCATCGTG GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTCTCTTCTGGAGGGGCAACCTT TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGCGAGTTCCGA AACCTGGCCTCCGGCGGTGCGGCCGCCGCCGCTCTCTCTTCGTGTACCCCGCTGGAT AACCTGGCCTCCGGCGGTGCGGCCGGCCGCCCCCTCTGCTTCGTGTACCCGCTGGAT AAGCAGATCTTCCTGGGGGGGGGTGGACAGACACGC---GTTCTGGAGGTACTTTGCGGGC AAGCAGATCTTCCTGGGGGGGGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGC GACTGCATTGTCCGCATCCCCAAGGAGCAGGGGGGTGCTGTCCTTCTGGAGGGGGCAACCTT Conservative 0; ω --465 297 405 237 345 180 285 120 225 60 165

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                                                                                                                                                                                                                                           Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
  The invention relates progression of liver of
                              Claim
                                               Diagnosing and detecting hepatocellular carcinoma involves detecting the leliver tissue sample -
                                                                                                                                                                                                           WO200229103-A2
                                                                                                                                                                                                                                                                                                                        ABN95598;
                                                                                                                                                                                                                                                                                                                                           ABN95598 standard;
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                             298pp; English.
 novel method for diagnosing r, hepatocellular carcinoma
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or metastatic liver
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                                                      GACTGTTGGAGGAAGATCTTCAGAGAGATGAGGGGGCAAGGCCTTCTTCAAGGGTGCGTGG
                                                                                          CGGCGCATGATGATGCAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTC
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                             TCCAACGTCCTGCGGGGCATGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGACCTCAAG
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                                                                                                                                                                                                                                             GGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAG
  AAGGTGATCTAA
                    TCCAACGTCCTGCGGGGCATGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAG
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777 885 717 825 657 645

477 585

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tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, and toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
Sequence 1116 BP; 231 A; 330 C; 346 G;
209 T; 0 other;
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GCCAACGTCATTCGCTACTTCCCCACTCAAGCCCCTCAACTTCGCCTTCAAGGATAAGTAC GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTT GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTGCTCCTTCTGGAGGGGCCAACCTT Pred. 0; Mis Score 771.2; Mismatches ö. 1e-149; 24; Ψ Indels Length 1116; ÿ Gaps 405 237 345 180 285 165 297 120 225 60

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ABL69347;

ABL69347 standard; DNA; 1116

15-MAY-2002 (first entry)

Prostate cancer related gene sequence SEQ ID NO:7684.

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25-SEP-2000;

26-SEP-2000;

27-SEP-2000;

27-SEP-2000;

27-SEP-2000;

27-SEP-2000;

27-SEP-2000;

28-SEP-2000;

28-SEP-2000;

28-SEP-2000;

28-SEP-2000;

28-SEP-2000;

28-SEP-2000;

29-SEP-2000;

29-SEP-2000;

29-SEP-2000;

29-SEP-2000;

29-SEP-2000;

20-OCT-2000;

02-OCT-2000;

03-OCT-2000;

03-OCT-2000;
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2000;
05-JUN-2000;
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                       (AVAL-) AVALON PHARM.
                                                                                                                              2000US-239113

2000US-231133

2000US-231034

2000US-234034P

2000US-23456P

2000US-23456P

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2000US-234924P

2000US-234924P

2000US-235087P

2000US-235134P

2000US-235134P

2000US-23563P

2000US-235720P

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Matches Query Match Best Local

Conservative

0;

99.28;

Score 771.2; DB 24; Pred. No. 1e-149; Mismatches

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Indels Length

Augustus M,

Carter KC,

Ebner R,

Endress G,

Horrigan S;

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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical ceasement to be tested for anti-neoplastic activity. determining a change in cexpression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL6164 cc comprises a sequence (S) selected from 8447 sequences (given in ABL6164 cc expression is indicative of anti-neoplastic activity. (I) has cytostatic cactivity and can be used in gene therapy. MI can be used for screening cc an anti-neoplastic agent, and can be used for producing a product which ci s the data collected with respect to the anti-neoplastic agent as a cc result of MI, and the data is sufficient to convey the chemical cc treatment of cancer such as colon, breast, stomach, lung, thyroid, cc oesophageal, ovarian, kidney, prostate or pancreatic cancer, infiltrating ductal cancer, ci infiltrating doublar cancer, squamous cell cancer, infiltrating ductal cancer, cc carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 7684; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soppet DR, Weaver Z;
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Sequence 1116 BP; 231 A; 330 C; 346 G; 209 T; 0 other;
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106 CTGCAGGTCCAGCACGCCAGCAAGCAGACAGTCGCCGCCGACAAGCAGTACAAGGGCATCGTG al Similarity 786; Conserv 346 AACCTEGCCTCCGGCGGTGCGGCCGGCGGCGCGCTCCCTCTGCTTCGTGTACCCGCTGGAT 405 286 AAGCAGATCTTCCTGGGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGC 345 418 526 238 181 226 GCCAACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCCTTCAAGGATAAGTAC 166 GACTGCATTGTCCGCATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTT 538 ATCGCGCAGACCGTGACGGCCGTGGCCGGCGTGTCCTACCCCTTCGACACGGTGCGG 61 Н AGCAGATCTTCCTGGGGGGCGTGGACAGACACGC---GTTCTGGAGGTACTTTGCGGGC GCCAACGTCATTCGCTACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTAC GACTGCATTGTCCGCATCCCCAAGGAGCAGGGGCGTGCTGTCCTTCTGGAGGGGCCAACCTT CTGCAGGTCCAGCACGCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTG GATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATG GGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTAC GGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGCATCCGGGGCCTGTACCAG 525 TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA 465 ATCGCGCAGACCGTGACGGCCGTGGCCGGCGTGTGTCCTACCCCTTCGACACGGTGCGG GATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATG GGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTAC GGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCCTGTACCAG TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA 297 237 180 120 225 60 477 417 357

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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndron PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                     Claim
                                                                                                                                                                                                                    Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer) immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-2000; 2000US-209467P
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DB; ABP43205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), end disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and to shock syndrome), inflammatory conditions (e.g., mastitis, oophorit vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematic management of the systemic lupus of themselves the systemic lupus of the systemic lupus
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GTGCAGGGCATCATCTACCGGGCGGCCGCCTACTTCGGCCGTGTACGATACGGCCAAGGGC
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                                                                                              CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC
                                                                                                                                                                                                CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAAGGCCTGGGAGACTGC
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                                                                       CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGNCTCC
                                                                                                                                                                      CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
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Pred. No. 3.1
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CC compounds or the progression of these toxic effects by determining the CC global changes in gene expression in tissues or cells exposed to the CC toxin and comparing these to gene expression in unexposed tissues or CC eells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the CC hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or CC more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of the toxic response and predict cellular pathways that a compound modulates the CC in a cell. The methods utilise a set of at least two probes (on a solid compound to the compound modulates specifically hybridises to a gene listed in the specification, a computer CC system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a cel set of genes comprising at least two genes listed in the specification, of a cel sited in the specification. The method is useful for at least one gene CC instead in the specification. The method is useful for at least one gene CC taisues or cell expression and for identifying the used as containing information used to present information containing information and for elucidating global containing information and for dentifying the used as containing information and containing information and toxicity markers in the problem of the physiological state of tissue or cell expression information of the physiological state of tissue or cell containing information and toxicity markers for the problem containing information and toxicity markers for the containing inc
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15-MAY-2001;
22-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat sequence differentially expressed in response to a hepatotoxin #1327.
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02-NOV-2000;
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2001US-290645P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 other;
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916 GGCATGGGGGGTGCTTTTGTATTGGTATTGTATGATGAGATCAAAAAATATGTGTAA
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                                     GGCATGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA
                                                                                                               ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG 840
                                                                                                                                                                           CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780
                                                                                                                                                                                                                                                                                                       ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
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                                                                       ATTGCAAAAGATGAAGGACGCAAAGCTTTCTTCAAAGGTGCTTGGTCCAACGTACTGAGA 915
                                                                                                                                                       CAGTCTGGCCGGAAAGGGGCTGATATTATGTACACGGGGACAGTTGACTGCTGGAGGAAG
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                                                                                                              The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying an insulin receptor signaling modulator, useful as ditargets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent
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2001US - 2614589

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                             GGCATGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA
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AAD00520 standard; CDNA; 897 ВP

AAD00520;

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT2 cDNA.

adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;

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(ANT) proteins of ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial diabetes and definess (MIDD), and myoclonic delectors, mitochondrial diabetes and definess (MIDD), and myoclonic depilepsy red ragged fibre syndrome. The present sequence is a CDNA encoding adenine nucleotide translocator ANT2 from human brain.
                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
                                                                                                                                                                                                                                                                                               Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression
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                                                                                                                                                                                                                                  78.9%;
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Pred. No. 2.4e-113;
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                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                   Human adenine nucleotide translocator-2 (ANT-2) cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                             AAS05902 standard; cDNA; 897 BP.
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07-SEP-2001 (first entry)

Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin; mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; /product= "ANT-2" Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes for human adenine nucleotide translocator-2 (C (ANT-2) protein. ANT proteins are mitochondrial permeability transport ctransition (MTP) pore components responsible for mediating transport cof ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to creat components responsible for mediating transport creating the MPT. The present invention relates to a novel nucleic acid components e.g. cyclophilins to core components e.g. cyclophilins to component protein nucleic acid components of the method are useful fore component polypeptide (c e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. ANT) fused to an energy transfer molecule (ETM) protein (c e.g. aNT) fused to an energy transfer molecule (ETM) protein (c e.g. aNT) fused to an energy transfer molecule (ETM) protein (c e.g. aNT) fused to an energy transfer molecule (ETM) protein (c e.g. aNT) fused to an energy transfer molecule (ETM) protein core components of luorescent protein (GPP) or a FLASH sequence). The novel c expression construct can alter mitochondrial membrane permeability c transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter C mPT and/or cell survival. These agents are useful for the prevention or c treatment of diseases associated with altered mitochondrial function or c dysfunctional cell survival, such as Alzheimer's disease, schizophrenia, c mitochondrial encephalopathy, lactic acidosis, stroke, c mitochondrial encephalopathy, lactic acidosis, stroke,
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Best Local S
Matches 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule.
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Velicelebi G,
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GGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.3%; Score 594.6; DB 22; 78.9%; Pred. No. 2.4e-113; tive 0; Mismatches 189;
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Db Qy	Qy Db	Qy Db	Db Oy	Db Qy	Db dg	Db Qy	DP QA	Db Qy
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1 GGCATGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA 897 	1 ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG 840 	1 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780 	ACGGCCGTGGCCGGCGTGGTGTCCTACCCCTTCGACACGGTGCGGCGGCGCGCATGATGATG 720	1 ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGATGATCGTGATGATCGCGCAGACCGTG 660 	1 GTGCAGGGCATCATCTACCGGGCGGGCGTACTTCGGCGTGTACGATACGGCCAAGGGC 600	L CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC 540 	L CTGGCAGCGGACGTGGGAAAGTCAGGGACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC 480 	GGTGCGGCCGGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCCAGAACCCGC 420
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Search completed: August 24, 2003, 02:53:16 Job time: 317 secs

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897
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BC013256 Homo sapi
BC035469 Homo sapi
BX419742 BX419742
AL545701 AL545701
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ECOL3256 LOCUS LOC	C C C C C C C C C C C C C C C C C C C
BC013256 BC013256 BC013256 BC013256.1 GI:15301544 SHTC. HOMO Sapiens (human) IISM Homo Sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Elikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CE 1 (bases 1 to 1355) RS Strausberg,R. Strausberg,R. Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remani: ATCC CONA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC	84.8 94.5 1201 9 AL534908 AL534918 BO922817 AGENCOURT BO92687 AL540267 AL539376 AL539376 AL539376 AL539376 AL539376 AL539376 AL539376 AL539376 AL539376 AL54027 AL540207 AL540

FEATURES

source

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://image.linl.gov Serles: IRAK Plate: 13 Row: e Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 3820534
This clone has the following problem: no 5' EST match.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
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Similarity 99.9%;
96; Conservative
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417 c 404 g 251 t
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Homo sapiens
                        Similarity
    Conservative
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1. 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Contact: A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg,R.
Direct Submission
Submitted (31-7UL-2002) National Institutes of Health, Mammalian Submitted (31-7UL-2002) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1355 bp
Homo sapiens, clone IMAGE:3867130,
BC035469
BC035469.1 GI:22028373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1355)
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                                                                                                                                                     /organism="Homo sapiens"
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/clone_tib="NHIDB"
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/note="myector: GAV-SPORM6"
/note="myector: GAV-SPORM6"
/note="myector: GAV-SPORM6"
Score 895.4;
Pred. No. 8.46
0; Mismatches
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                          sapiens
                                      sapiens (human)
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 ; Metazoa;
Eutheria;
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5-PRIME, mRNA sequence.
Chordata;
Primates;
Craniata; Vertebrata; Catarrhini; Hominidae;
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Best Local Similarity
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Contact: Genoscope
Genoscope - Centre National de 9
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Faraday Avenue Genoscope sequence ID : CSODF020BB08QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgi-bin/cluster.cgi?seq-CSODF020BB08QP1&cluster-10389.r. Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library was constructed by Life Technologies, invitrogen. This sequence belongs to sequence more information about this cluster, see http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1201)
Li, W.B., Gruber, C.,
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                                                           CTGGCAGCGGACGTGGGAAAĞTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
                                                                                                               GGTGCGGCCGGCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC
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                        CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC
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            CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCMTGTACCAGGGCTTCAGTGTCTCC
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/db_xref="taxon:9606"
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/tissue_type="FETAL BRAIN"
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/clone_ilb="Homo sapiens FETAL BRAIN"
/clone_ilb="Homo sapiens FETAL BRAIN"
/clone_ilb="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pcMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pcMVSPORT 6
vector. Library was not normalized."
45 a 365 c 354 g 210 t 27 others
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Pred. No. 7.6e
11; Mismatches
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Technologies, a division o
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/.6e-175;
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	BASE COUNT	FEATURES SOUICE	JOURNAL COMMENT	REFERENCE AUTHORS TITLE	RESULT 4 AL545701 LOCUS DEFINITION ACCESSION	QY QY Db	Qy Db Qy	Оу Оу Оу
y Match 94.8%; Score 850.8; DB 9; Length 1201; Local Similarity 98.8%; Pred. No. 3.3e-173; hes 878; Conservative 0; Mismatches 8; Indels 3; Gaps 2;	2248			EST. Homo sapiens (human) M Homo sapiens (Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201) Jessee, J. and Polayes, D. Li.W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length coNA libraries and normalization	AL545701 AL545701 Hom clone CSODIC AL545701	780 GATCTTCAGAGATGAGGGGCAAGGCCTTCTTCAAGGGTGCTGGTCCTAACGTCCTGCG 839	660 GACGGCCGTGGCGGCGGGTGTTGCTACCCCTTCGACACGGTGCCGCGCGCATGATGAT 719	541 GTGCAGGGCATCAT-CATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGG 599
KEYWORDS SOURCE ORGANISM	RESULT 5 AL534908 LOCUS DEFINITION ACCESSION VERSION	Db Db	0y 0y 0y	ОУ ОУ ОУ	0y 0y 0b	Qy Db	ОУ ОУ ОУ	Оу Оу Оу
¥	AL534908 1201 bp mRNA linear EST 12-MAY-2003 ON AL534908 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF007YI20 5-PRIME, mRNA sequence. N AL534908 AL534908.2 GI:30541165	778 GCAAAGGAGCTGACATCTACACGGGCA-CGTCCACTGTTGGAGGAACATCTTCAGAG 836 791 ATGAGGGGGCAAGGCCTTCTTCAAGAGGTGCTGGTCCAACGTCCTGCGGGGCATGGG 848	611 ACCCCAGACACCCCCTCGTGGTGACCTGATGATCGCCAGACCCGTGACGCCCGTGG 70	TCATCATCTACCGGGCGCTACTTCGGGCGTGTACAGGCATCAAGGCATGCAGGCATGCAGGCAAGTCCAAGGCATCAAGGCATCACGGCAAGGCATCAAGGCATCAAGGCATCAAGGCATCAAGGCATCAAGGCATCAAGGCATCAAGGCATCAAGGCATGCAAGGCATGCAGGCATGCAAGGCATGCAAGGCATGCAGGCATGCAAGGCATGCAAGGCATGCCAGGCATGCCAGGCATGCTCAAGGGCATGCCAAGGGCATGCCCCGTTTACTACCAGGCAAGAGGCATGCTCACGGCATGCTAACGGCAAGGCATGCTCCCCGTTTTACTACCAGGCAAGAGAGATAACGGCAAGGCATGCTCCCCGTTTTACTACCAGGCAAGAGGCATGCTCCCCGTTTACTACAGGAAGAGGCAAGAGAAGAGAAGAAGAAGAAGAAGAAG	371 GCGCGACCTCCCTCTGCTTCTGTACCCGCTGGATTTTGCCAGAACCCGCCTGGCAGCGG 430	251 CTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTGGGGGGGG	131 AGATCGCCGCCGACAACAGTACAAGGCATCGTGGACTGGCATTGTCCGCATGCTCAAGG 190 111 1 1 1 1 1 1 1 1 1 1 1 1	

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On Feb 13, 2001 this sequence version replaced gi:12798401.
Contact-Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF007BE10QP1&cluster=10389.r. Contact
cgi-bin/cluster.cgi?seq=CSODF007BE10QP1&cluster=10389.r. Contact
cgi-bin/cluster.cgi?seq=CSODF007BE1039.r. Contact
feng Liang Email: fliang@llfeterout URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF007BE10QP1.
Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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GGTGCGGCCGGCCGACATCCCTCCTCCTCCTGTGTGTACCCGCTGGATTTTTGCCAGAACCCGC
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF007Y120"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-Oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
a 374 c 357 g 214 t 16 others
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BASE COUNT ORIGIN	ALL CE		Оу 8, Оъ 9!	Qy 781 Db 938	Qy 721 pb 879	Qy 661 Db 819	Qy 601 Db 759	Qy 541 Db 699
172 a 305 c 297 g 173 t 2 others	aplens lapiens la; Metazoa; Chordata; Craniata; Vert la; Eutheria; Primates; Catarrhini; Ho cses 1 to 949) cses 1 to 949 cses 1	NN = UN	41 GGCAT-GGGGGGGGCCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA 897 	31 ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG 840 	21 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780 	61 ACGGCCGTGGCCGGCGTGGTGTCCTACCCCTTCGACACGGTGCGGCGGCGCGCATGATGATG 720 11	01 ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG 660	41 GTGCAGGGCATCATCATCTACCGGGGGGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC 600

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Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13324 row: 1 column: 19
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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                                                                          CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGGTTCCGAGGCCTGGGAGACTGC
                                                CTGGCAGCGGACGTGGGAAAGTCAAGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
                                                                                                   GGTGCGGACGCGCGCTCTCTGCTTCGAGTACCCGCTGGATTTCGCCAGAACCCGC
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ilarity 96.7%;
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                                                                                                                                                                                                    Email: sequence cons.fr. Web: www.genoscope.cns.fr was not normalized. Library was constructed by Life Technologies, division of Invitrogen. This sequence belongs to sequence cluster 10389.r For more information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq~CSODF032CG01QF1&cluster=10389.r. Contact: Peng Liang Email: fliang@lifetech.com URL: http://tullength.invitrogen.com/InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODF032CG01QF1.
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AL540267 Homo
CS0DF032YN01
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1 (bases 1 to 1201)
L1,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de
BP 191 91006 EVRY cedex - Franc
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    /Clone_lib-"Homo sapiens FETAL BRAIN"
/rote="Organ: brain; Vector: pCMVSPORT_6; 1st s
/mote="Organ: brain; Vector: pCMVSPORT_6; 1st s
/mas primed with a NotI-oligo(dT) primer. Five p
enriched, double-strand cDNA was digested with
cloned into the Not I and EcoRV sites of the pc
vector. Library was not normalized."

349 c 357 g 218 t 28 others
                                                                                                                                 /db_xref="taxon:9606"
/clone="CS0DF032YN01"
                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                         /tissue_type="FETAL BRAIN"
/dev_stage="fetal"
                                                                                                                                                                                           Location/Qualifiers
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1 ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCCGCCGCCGCCGAGGAACACACGCCATCTCCTTCGCCCAAAGACTTCTTGGCCGGAGG-ATCGCCGCCGCC
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seqcSODF033AH100p1&cluster=10389.r. Contact:
freng Liang Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF033AH10QP1.
Location/Qualifiers
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1 (bases 1 to 1201)

11,W.B., Gruber, C., Jessee, J. and Polayes, D.

11,W.B., Gruber, G., Jessee, J. and Polayes, D.

12,W.B., Gruber, G., Jessee, J. and Polayes, D.

12,W.B., Gruber, G., Jessee, J. and Polayes, D.

12,W.B., Gruber, G., Jessee, J. and Polayes, D.

13,W.B., Gruber, G., Jessee, J. and Polayes, D.

14,W.B., Gruber, G., Jessee, J. and Polayes, D.

14,W.B., Gruber, G., Jessee, J. and Polayes, D.

15,W.B., Gruber, G., Jessee, J. and Polayes, D.

16,W.B., Gruber, G., Jessee, J. and Polayes, D.

16,W.B., Gruber, G., Jessee, J. and Polayes, D.

17,W.B., Gruber, G., Jessee, J. and Polayes, D.

17,W.B., Gruber, G., Jessee, J. and Polayes, D.

18,W.B., Gruber, G., Jessee, J. and P
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Homo sapiens
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                                                                   CTGGCAGCGGACGTGGGAAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC 480
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CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCCTGGGAGACTGC
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/mol_type="mRNA"
/mb_xref="taxon;9606"
/db_xref="taxon;9606"
/clone="CSODE033Y019"
/tlssue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pcMVSPORT_6; lst strand cDNA
/note="Organ: brain; Vector: pcMVSPORT_6; lst strand cDNA
was primed with a Not!-oligo(dT) primer: Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pcMVSPORT 6
vector. Library was not normalized."
42 a 358 c 360 g 221 t 20 others
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Pred. No. 1.1e-168;
3; Mismatches 5; Indels 5;
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T CEL CONA DE ENDA	de Sequencage ance fr, Web : www.genoscop was constructed by Lif sequence belongs to s about this cluster, s H003CB10QP1&cluster=10 fetech.com URL : .com/ InVitroGen Corpo uence ID : CSODH003CB1	J. and Polayes,D. and normalization ce version replaced gi:129	EST: OFFICE (human) HOmo sapiens (human) Homo sapiens (human) Eukaryota: Meresaca: Chordata: Craniata: Vertebrata: Euteleostomi; Eukaryota: Meresaca: Deimata: Office (human)	AL557414 Momo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA clone CSODH003YD19 5-PRIME, mRNA sequence. AL557414 GT:31778214	O1	99 GGGCATGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA 897	0 GATCTTCAGAGATGA-GGGGGCAAGGCCTTCTTCAAGGGTGCGTGCGTGCCAACGTCCTGC 838	21 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTT-GGAGGAA 779 	61 ACGGCCGTGGCCGGCGTGGTGTCCTACCCCTTCGACACGGTGCGGCGGGCG	01 ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG 660	97 GTGCAGGGCATCATCATCTACCGGGCGGCCTACCTCGGCGTGTACGATACGGCCAAGGGC 756	CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCCC	1 CTGGTGAAGATCACCAAGTCCGACGGCCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC 5

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AL514420 Homo sapiens
CLOBBO10ZFO1 5-PRIME,
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                                                                                                  ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belong to sequence cluster 10389.r
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB010ZF01RP1&cluster=10389.r. Conta
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB010ZF01RP1.
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Full-length cDNA libraries
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                                           GGTGCGGCCGCGACCTCCCTTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC
                                                                                                   GGGGGCTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC
                                                                                                                                          TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
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                                                                                    GGGGGCGTGGACAAGCACGCAGTTCTGGAGGTACTTTGCGGGCCAACCTGGCCTCCGGC
                            GGTGCGGCCGCGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTCGCCAGATCCCGC
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346 c 370 g 219 t 33 others
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/mol_type="mRNA"
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7; Mismatches
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/Cloue_ILD="All_Moc_gos" / Porton: pCMV-SPORT6; /note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."	/db_xref""taxon:9606" /clone="IMAGE:5736668" /tlasue_type="duodenal adenocarcinoma, cell line" /lab_host="DH10B (phage-resistant)"	FEATURES Location/Qualifiers Source 11071 /organism="Homo sapiens" /mol.type="mRNA"	sortium/LLNL at: : 05	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MCC clone distribution information can be	AL Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC	Eutheria; Primates; Catarrhini; Hominidae; 1 to 1071) tp://mgc.nci.nih.gov/. nstitutes of Health, Mammalian Gene Collec	S EST. Homo sapiens (human) ISM Homo sapiens Eukaryota; Metazoa; Chordata;	<pre>ITION AGENCOURT_6545407 NIH_MGC_88 Homo sapiens cDNA clone 5', mRNA sequence. SION BM554606 ON BM554606.1 GI:18794346</pre>	bo mRNA linear EST	QY 841 GGCATGGGGGCCCCTTCGTGCTGGTCCTGTACGA 875	Qy 781 ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG 840	Qy 721 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780	Qy 661 ACGCCGTGGCCGCGTGGTGTCCTACCCCTTCGACACGCTGCGCGCGC	Qy 601 ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAAGATCGATGATCGCGCAGACCGTG 660	Qy 541 GTGCAGGGCATCATCTACCGGGGGGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC 600	QY 481 CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC 540	
RESULT 13 BX375536 BX375536 BX375536 BX375536 BX375536 HOMO SAPIENS NEUROBLASTOMA COT 25-NORMALIZED HOMO SAPIENS CDNA clone CS0DC014YG24 5-PRIME, mRNA sequence.	QY 838 CGGGGCATGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGGTCCTAAGAAGGTG 891	Qy 780 GATCTTCAGAGATGA-GGGGGGCAAGGCCTTCTTCAAGGGTGCGT-GGTCCAACGTCCTG 837	Qy 721 CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTT-GGAGGAA 779	QY 661 ACGCCGTGGCCGGCGTGGTGTCCTACCCCTTCGACACGGTGCGGCGCGCATGATGATG 720	Qy 601 ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG 660	Qy 541 GTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC 600	Qy 481 CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC 540	Qy 421 CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGGAGATTCCGAGGGCCTGGGAGACTGC 480	Oy 361 GGTGGGGCGGGGGACCTCCCTCTGCTTCGTGTAGCCGGTAGATTTGCCAGAAACCCGC 420	QY 301 GGGGGCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC 360	QY 241 TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG 300	QY 181 ATCCCAAGGAGCAGGGGGTGCTGTCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC 240	QY 121 GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC 180	Qy 61 ATCTCCAAGACGGCCGTGGGTCCAGTCGAGCGGGTCAAGCTGCTGCAGGTCCAGGAC 120	Qy 1 ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCCC 60	Query Match 90.9%; Score 815.2; DB 12; Length 1071; Best Local Similarity 97.2%; Pred. No. 1.5e-165; Matches 873; Conservative 0; Mismatches 18; Indels 7; Gaps 4;	BASE COUNT 214 a 335 c 334 g 187 t 1 others ORIGIN

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Email: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genoscope.cns.fr/
cgi-bin/cluster-cgi?seq=CSODCO14BD12QP1&cluster-10389.r.
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID: CSODCO14BD12QP1.
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1 (bases 1 to 1014)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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/mol_type="mRNA"
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Tissue Procurement: DCTD/DTP/Gazdar
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National Institutes of Health, M
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                    /Clone="IMAGE:6424804"
/tissue_type="large cell carcinoma"
/tissue_type="large cell carcinoma"
/lab_host="Du108 (phage-resistant)"
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1 (bases 1 to 1201)

1 (Juases 1 to 1201)

2 (Juas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGACGGAACAGGCCATCTCCTTCGCCAAAGACTTCTTGGCCGGAGGCATCGCCGCCGCC
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cgi-bin/cluster-gi?seg-cslAF009ZD08QPl&cluster=10389.r.
Feng Liang Email : fliang@lifetech.com URL :
Feng Liang Email : fliang@lifetech.com/CINICOGEN COMPORATION
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID : CSIAF009ZD08QPl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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ilarity 97.2%;
Conservative
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/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pcMVSPORT_6; lst strand cDNA
/note="Organ: brain; Vector: pcMVSPORT_6; lst strand cDNA
was primed with a NotI-ollgo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pcMVSPORT 6
vector. Library was not normalized."
vector. Library was not normalized."
215 t 29 others
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Pred. No. 4.1e-164;
3; Mismatches 17;
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Search completed: August 24, 2003, 03:33:47 Job time: 2423 secs

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RESULT 2
US-09-620-312D-687
FILE REFERENCE: 784C1P2B

CURRENT APPLICATION NUMBER: US/09/620,31

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105
                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: L1u, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Lao, Qing A.
APPLICANT: Wach, Jing A.
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el NUTILE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2h
                                                                                                                                                                                                                                                                                                                            Sequence 687, Applica Patent No. 6569662 GENERAL INFORMATION:
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LENGTH: 1
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LOCATION: (131)..(1027)
-09-620-312D-687
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ORGANISM:
FEATURE:
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 GGCATGGGGGGGCGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAGAAGGTGATCTAA
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Title:
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Maximum Match 100%
Listing first 45 summaries
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2. /cgn2_6/ptodata/2/lna/6A_COMB.seq:*

3. /cgn2_6/ptodata/2/lna/6A_COMB.seq:*

4. /cgn2_6/ptodata/2/lna/6B_COMB.seq:*

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Patent No. 555536

GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Murphy, Anne N.
APPLICANT: Miley, Sandra Elleen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigerl, Juciano G.
APPLICANT: Patel Calebi, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE REFERENCE: 660088, 433
CURRENT APPLICATION UNDER: US/09/434,354
CURRENT APPLICATION UNDER: US/09/434,354
SOSTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 3
LENGTH: 897
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                                                                                                                                      ATCCCCAAGGACCAGGCGTGCTGTCCTTCTGGAGGGCAACCTGCCAAGGTCATTCGC
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US-09-434-354-2
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
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CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS; AND FOR TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS FILE REFERENCE: 660088.433
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                                                                                                                  CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTTCAGTGTCTCC
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ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
                                                                                               CTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTAACGTGTCT
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-961-871-11
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                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-9;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8080
TELEFAX: (303) 499-8080
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08961871
Patent No. 6013858 ISSUED 01.11.00
GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 706; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wallace, Douglas C.
APPLICANT: MacGregor, Grant R.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 3]-OCT-1997
CLASSIFICATION: 800
                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 5370 M
CITY: Boulder
STATE: Colorad
COUNTRY: US
                                                                                                                                                                 STRANDEDNESS: double TOPOLOGY: not relevant
                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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     Conservative
                                                                                   190.
                                                                                                                                                   DNA (genomic)
               65.98;
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                                                                                                                                                                                                                                                                                                                      78-96
Score 591.4; Pred. No. 4.2e
0; Mismatches
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                 4.2e-1
   DB 3;
2e-122;
191;
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                                Length 1259;
0;
Gaps
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Sequence 9, Application US/08961871 Patent No. 6013858 GENERAL INFORMATION:
APPLICANT: Mallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
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APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: FELDEY, DONA M.
REGISTRATION NUMBER: 78-96
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPAX: (303) 499-8080
TELEPAX: (303) 499-8080
TELEPAX: (303) 499-8089
INFORMATION FOR SED ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGIH: 1177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ORGANISM: MUS musculus
FEATURE:
LENGINGE: CDNA to mRNA
HYPOTHETICAL: NO
ORGANISM: MUS musculus
FEATURE:
LENGINGE: LONG TO MENTAL SOURCE:
LENGINGE: CDNA TO MRNA
HYPOTHETICAL: NO
ORGANISM: MUS musculus
LENGINGE: LENGINGE:
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Best Local
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STREET: 5370 Manhattan
CITY: Boulder
STATE: Colorado
COUNTRY: US
2IP: 80303
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                            454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                        GGTGCGGCCGGCGGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC 180
                            GGGGCAGCTGGGGCCACCTCCCTCTGCTTCGTCTACCCGCTGGACTTTGCTAGGACCACG
                                                                                                                                                GGAGGCGTTGATCGACATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCCTCTGGT 453
                                                                                                                                                                                   GGGGCCGTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCTCCGGC 360
                                                                                                                                                                                                                                                                    TACTTCCCCACTCAAGCCCTGAACTTCGCCTTCAAAGACAAGTACAAGCAGATCTTCCTG
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94..990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.6%;
78.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 588.2; DB 3;
Pred. No. 2.1e-121;
0; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #1.30
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application Patent No. 6562563 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
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CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                              PATENT NO. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION
TITLE OF INVENTION: PATHMAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 622, Appl Patent No. 6500938
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for 1
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                                                                                                                     STREET: 3174 PORT
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Sequence 38, Application US/08518878B Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
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Best Local Similarity 99.5%;
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 97.01
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 622:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tartagila, Louis A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
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APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   STREET: 1155 AVECITY: New York
STATE: New York
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CLONE: 2517151
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 10036-2711
                             CLASSIFICATION:
                                                   APPLICATION NUMBER: FILING DATE: 23-AU
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1155 Avenue of the Americas
                                23-AUG-1995
DN: 435
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                                                                      US/08/518,878B
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Pred. No. 1.2e-32;
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TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38, Application US/08294522B Patent No. 5741666 GENERAL INFORMATION:
  STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 788
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
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(212) 869-97
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1155 Avenue of the Americas
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ADDRESSEE:

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                                                                                                                                                                                                                                   Sequence 38, Application US/08470868A Patent No. 5861485
GENERAL INFORMATION:
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Best Local Similarity 45.6%;
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TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
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FILING DATE: 23-AUG-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                            APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                       ZIP: 10036
                                                        COUNTRY:
                                                                                                              STREET:
                                                                                                                             ADDRESSEE:
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                                                                                            New York
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                                                                           New York
                                                                                                              1155 Avenue of the Americas
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                                                          USA
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Pred. No. 0.00074;
0; Mismatches 236;
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RESULT 11
US-08-807-861A-38
; Sequence 38, Application US/08807861A
; Patent No. 5853975
; Patent No. 5853975
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                                                                                                            GENERAL INFORMATION: APPLICANT: Tartag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                            TITLE OF INVENTION: ME
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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STREET:
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SOFTWARE: Patentl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/470,868A FILING DATE: 06-JUN-1995
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                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                             501
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                                                                                                                                                                                                                                                                            876 CGAGCTCAAGAAGG
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                                                                                                                                                                                                                                                                                                                                         GGGTGCGTGGTCCAACGTCCTGCGGGGCATGGGGGGGCGCCTTCGTGCTGGTCCTGTACGA
                                                                                                                                                                                                                                                                                                                                                                           AAGCACCGTCAATGCCTACAAGACCATTGCCCGAGAGGAAGGGTTCCGGGGCCTCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCCTGTATGATTCTGTCAAACAGTTCTACACCAAGGGCTCTGAGCATGCCAGCATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCGTGTACGATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGT
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                                                                                                                                                                                                                                            TGACCTCATCAAGG
                                                                                                                                                                                                                                                                                                           AGGGACCTCTCCCAATGTTGCTCGTAATGCCATTGTCAACTGTGCTGAGCTGGTGACCTA
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           3: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                      Tartaglia, Louis A.
VENTION: METHODS AND COMPOSITIONS FOR THE
VENTION: REGULATION OF BODY WEIGHT DISORDERS,
EQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 790-90
(212) 869-8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.3%;
45.6%;
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Pred. No. 0.00074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #1.30
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                                                                              INCLUDING
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US-08-807-861A-38
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TELEPHONE: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.3%; Score 56.4; DB 2; Length 1596; Best Local Similarity 45.6%; Pred. No. 0.00078; Matches 198; Conservative 0; Mismatches 236; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/518,878
APPLICATION NUMBER: US 08/470,868
APPLICATION NUMBER: US 08/294,522
APPLICATION NUMBER: US 08/294,522
APPLICATION NUMBER: US 08/294,522
APPLICATION NUMBER: J3-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LABITA A.
REGISTRATION NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DALL.
CLASSIFICATION: 51.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
APPLICATION NUMBER: 23-AUG-1995
US 08/470,869
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                            663 GAGCCGCCTCCTAGCAGGCAGCACCACAGGTGCCCTGGCTGTGGCTGTGGCCCAGCCCAC 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             603
903 TGACCTCATCAAGG 916
                                                   876 CGAGCTCAAGAAGG 889
                                                                                                       843 AGGGACCTCTCCCAATGTTGCTCGTAATGCCATTGTCAACTGTGCTGAGCTGGTGACCTA 902
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10036-2711
                                                                                                                                                                                                                                                                AAGCACCGTCAATGCCTACAAGACCATTGCCCGAGAGGAAGGGTTCCGGGGCCCTCTGGAA 842
                                                                                                                                                                                                                                                                                                                                                                                        CACGGTGCGGCGCGCATGATGATGCAGTCCGGGCGCAAAGGAGCTGACATCATGTACAC 755
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                                                                                                                                                           GGATGTGGTAAAGGTCCGATTCCAAGCTCAGGCCCGGGCTGGAGGTGGTCGGAGATACCA 782
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US-09-210-681-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 7853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOTECTIC TYPE: DATE
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GENERAL INFORMATION:
APPLICANT: Tartag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.3%;
Best Local Similarity 45.6%;
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
ETLING DATE: 23-AUG-1995
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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696 CACGGTGCGGCGCGCATGATGATGCAGTCCGGGCGCAAAGGAGCTGACATCATGTACAC 755
                                                     663 GAGCCGCCTCCTAGCAGGCAGCACCACAGGTGCCCTGGGCTGTGGCCTGTGGCCCAGCCCAC 722
                                                                                                       636 GAGCTGGATGATCGCGCAGACCGTGACGGCCGTGGCCGTGGTGTCCTACCCCTTCGA 695
                                                                                                                                                                                                     576 CGGCGTGTACGATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGT 635
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                                                                                                                                                                                                                                                          543 CCTCTACAATGGGCTGGCTGCCGGCCTGCAGCGCCAAATGAGCTTTGCCTCTGTCCGCAT 602
                                                                                                                                                      CGGCCTGTATGATTCTGTCAAACAGTTCTACACCAAGGGCTCTGAGCATGCCAGCATTGG 662
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Pred. No. 0.00078;
0; Mismatches 236; Indels 0
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US-08-946-719A-38
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                                                                                                                                                     ; MOLECULE TYPE: US-08-946-719A-38
                                                            Query Match
Best Local Similarity 45.6
Conservative
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Patent No. 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOK AFFIANCE US 08/0
APPLICATION NUMBER: US 08/0
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/0
PTITING DATE: 23-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/470,868 FILING DATE: 06-JUN-1995 APPLICATION NUMBER: US 08/294,522 FILING DATE: 23-AUG-1994
                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 8-CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                      TOPOLOGY:
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   483 CCAGTACCGCGGTGTGATGGGCACCATTCTGACCATGGTGCGTACTGAGGGCCCCCGAAG
                                     456 CGAGTTCCGAGGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGACGGCATCCGGGG 515
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E: New York
TRY: U.S.A.
10036-2711
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                   (212)
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26-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BODY WEIGHT DISORDERS,
                                                                                            45.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.30
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                                                                          Score 56.4; DB 3; Pred. No. 0.00078; 0; Mismatches 236;
                                                                                                            Length 1596;
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   INFORMATION
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,983
FILING DATE: 12-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDI
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                             APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
TELEFAX: (61)
TELEX: 661
ON FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                        NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGGACCTCTCCCAATGTTGCTCGTAATGCCATTGTCAACTGTGCTGAGCTGGTGACCTA
                                                                                         REFERENCE/DOCKET NUMBER:
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                                     (212)
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55 Avenue of the Amer
   PENNIE
NO: 38
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TITLE OF INCHESTOR

TITLE OF INCHESTOR: NOVEL COMPOUNDS

FILE REPERENCE: GH-30002

CURRENT APPLICATION NUMBER: US/09/142,565A

CURRENT FILING DATE: 1999-06-30

EARLIER FILING DATE: 1997-03-05

EARLIER FILING DATE: 1997-03-05

EARLIER FILING DATE: 1997-03-05

EARLIER FILING DATE: 1997-03-05

EARLIER FILING DATE: 1997-07-18

EARLIER FILING DATE: 1997-07-16

NUMBER OF SEG ID NOS: 6

SOFTWARE: PASHSEO FOR WINDER: 97305305.1

EARLIER FILING DATE: 1997-07-16

NUMBER OF SEG ID NOS: 6

SOFTWARE: PASHSEO FOR WINDOWS VERSION 3.0

SEQ ID NO 1

LENGTH: 1192

TYPE: DNA

ORGANISM: HOMO SAPIEN

US-09-142-565-1
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LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 11near
NOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-547-983-38
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US-09-142-565-1
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GENERAL INFORMATION:
APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
APPLICANT: Kelly Paine
APPLICANT: ROBERT James
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Best Local Similarity 45.6%;
Matches 198; Conservative
Query Match
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  6.0%;
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     Score 54.2;
     DB 3;
     Length 1192;
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788 TGGTGACCTACGACATCCTCAAGGAGA 814
                                          866 TCCTGTACGACGAGCTCAAGAAGGTGA 892
                                                                                                                                                                                   608 CAGATGTGGTGAAGGTCCGATTTCAGGCCCAGCATACACCTCGGGCCATCCAGGAGCGACA 667
                                                                                                                                                                                                                                                                                                                        686 ACCCCTTCGACACGGTGCGGCGCGCATGATGATGCAGTCCGGGCGCAAAGGAGCTGACA 745
                                                                                                                                                                                                                                                                                                                                                                         548 CTACCCGGATTTTGGCCGGCTGCACCACAGGAGCCATGGCGGTGACCTGTGCCCAGCCCA 607
                                                                                                                                     GCCTGTGGAAAGGAACTTTGCCCAACATCATGAGGAATGCTATCGTCAACTGTGCTGAGG
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Search completed: August 24, 2003, 05:34:13 Job time: 77 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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Maximum Match 100%
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    1:
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110::
113::
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897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                 : /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS.PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compug
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Query Match Length	DB	ID	Description
ב	897	100.0		9	US-09-811-094-3	Sequence 3, Appli
2	897	100.0	897	9	US-09-810-644-3	
w	897	100.0		10	US-09-185-904A-3	
4	895.4	99.8		14	US-10-037-270-687	Sequence 687, App
₅	873.4	97.4		13	US-10-044-090-152	Sequence 152, App
6	771.2	86.0		10	US-09-969-708-213	Sequence 213, App
7	771.2	86.0		10	US-09-880-107-2096	Sequence 2096, Ap
8	771.2	86.0		14	US-10-171-581-48	Sequence 48, Appl
9	596.2	66.5		10	US-09-917-800A-1327	
10	594.6	66.3		9	US-09-811-094-2	Sequence 2, Appli
11	594.6	66.3		9	US-09-810-644-2	Sequence 2, Appli
12	594.6	66.3		10	US-09-185-904A-2	Sequence 2, Appli
13	581.8	64.9		14	US-10-198-846-13437	Sequence 13437, A
14	564.2	62.9		9	US-09-811-094-1	Sequence 1, Appli
15	564.2	62.9		9	US-09-810-644-1	Sequence 1, Appli
16	564.2	20	000	3		

18 429 47.8 468 11 US-09-918-995-26014 19 412 45.9 493 11 US-09-918-995-1953 20 394 43.9 720 9 US-09-910-943-105 21 392.4 43.7 410 11 US-09-918-995-16539 22 363.2 40.5 4460 11 US-09-918-995-15524 23 334 37.2 420 11 US-09-918-995-5524 24 318.6 35.5 413 11 US-09-918-995-35706 25 318.4 35.5 413 11 US-09-918-995-17465 26 317 35.3 409 9 US-09-928-301-617 27 306 34.1 424 11 US-09-918-995-17465 28 302.8 33.8 501 9 US-09-938-995-17465 29 299 33.3 390 11 US-09-918-995-37003 31 296.4 31.9 402 11 US-09-918-995-37003 31 282.2 31.5 483 11 US-09-918-995-37381 33 282.2 31.5 483 11 US-09-918-995-37381 34 278.8 31.1 408 10 US-09-918-995-37981 35 278.8 31.1 408 10 US-09-918-995-37948 36 278.3 3.0 487 9 US-09-918-995-37948 37 274.3 30.7 324 10 US-09-918-995-37948 38 266.4 29.7 417 11 US-09-918-995-5864 40 265.8 29.5 484 11 US-09-918-995-58794 41 264.6 29.5 485 11 US-09-918-995-58794 42 264.2 29.5 484 11 US-09-918-995-58794 43 240.4 26.8 1536 9 US-09-864-761-3148 44 240.4 26.8 1536 9 US-09-864-761-3148 45 226 25.2 927 14 US-1-128-714-2338
47.8 468 11 43.9 43.1 11 43.7 410 11 37.2 420 11 35.5 434 10 35.5 439 9 0 34.1 424 11 33.3 390 11 33.3 390 11 33.3 416 11 33.3 416 11 31.9 483 11 31.9 483 11 31.1 408 10 31.1 408 10 31.
.8 468 11 .9 720 9 0 .7 460 11 .5 434 10 .5 434 10 .5 434 10 .5 434 11 .3 409 9 0 .1 424 11 .3 390 11 .3 416 11
US-09-918-995-26014 US-09-918-995-9153 US-09-910-943-105 US-09-918-995-16539 US-09-918-995-5524 US-09-918-995-5524 US-09-918-995-3706 US-09-918-995-17465 US-09-925-301-617 US-09-918-995-17465 US-09-918-995-37003 US-09-918-995-37003 US-09-918-995-37381 US-09-918-995-1495 US-09-918-995-1496 US-09-918-995-1496 US-09-918-995-14747 US-09-918-995-37948 US-09-918-995-37948 US-09-918-995-37948 US-09-918-995-37948 US-09-918-995-6070

ALIGNMENTS

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; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-811-094-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Schob, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MOOS, Walter H.

APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
  2
                   61 ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC 120
                                                                          ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC 120
                                                                                                                                                           100.0%; Score 897; DB 9; ilarity 100.0%; Pred. No. 5.3e-227; Conservative 0; Mismatches 0;
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Sequence 3, Application US/09810644

Patent No. US20020012992A1

GENERAL INFORMATION:
APPLICANT: Naderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Scott W.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088:420D3

CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILENG DATE: 2001-03-14
  US-09-810-644-3
IS-09-810-644-3
Sequence 3, App.
Patent NO. US2
GENERAL INFORM
APPLICANT: An
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Best Local S
Matches 897
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SEQ ID NO 3
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ORGANISM: Homo
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                                                                                                                                                                                                CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG 780
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                                                                                                                                  ATCTTCAGAGATGAGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGGTCCAACGTCCTGCGG 840
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APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NU
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088 420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
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Best Local
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TYPE: DNA
ORGANISM: Homo sapien
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GTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTACGATACGGCCAAGGGC
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100.0%; Pred. No. 5.3e-227;
tive 0; Mismatches 0;
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DR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
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RESULT 4
US-10-037-270-687
Cequence 687, Ap
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(1027)
US-10-037-270-687
                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 687
LENGTH: 1212
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                                                                                                                                   Query Match
Best Local Similarity
Matches 896; Conserv
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TITLE OF INVENTION: NO. US20030104529Alel Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
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                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                 Chen, Rui-hong
Chen, Qing A.
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
Tillinghast, John
                                  ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC
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Chen, Rui-hong
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Zhang, Jie
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Pred. No. 1.4e
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hes 1;
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                                                                                                                                                           Length 1212;
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WS-10-044-090-152
US-10-044-090-152
US-10-044-090-152
Sequence 152, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVERVION GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILLE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILLING DATE: 2002-01-09
NUMBER OF SEQ ID NOS:-850
SEQ ID NO 152
SEQ ID NO 152
SEQ ID NO 152
FEATURE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unissufe
OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11
NAME/KEY: unissufe
LOCATION: 1131, 1929
OTHER INFORMATION: a, t, C, g, or other
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       Sequence 213, Application US/09969708
Patent No. US20020102532A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
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Pred. No. 9.9e-221;
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PATENTIN VERSION 3.0
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CURRENT FILLING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
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TYPE: DNA
ORGANISM: Homo sapiens
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              TCCAACGTCCTGCGGGGGATGGGGGGGGGCCTTCGTGCTGGTCCTGTACGACGAGCTCAAG
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APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-WO
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-01-14
PRIOR PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEO ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
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Matches 786
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APPLICANT: Vockle
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OTHER INFORMATION: Genbank Accession
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GATACGGCCAAGGGCATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATG
                                                                                                                                                                                                                                             GGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTAC
                                                                                                            GGCCTGGGAGACTGCCTGGTGAAGATCACCAAGTCCGGACGCATCCGGGGCCTGTACCAG
                                                                                                                                                              TTTGCCAGAACCCGGCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA
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                                                GGCTTCAGTGTCTCCGTGCAGGGCATCATCATCTACCGGGCGGCCTACTTCGGCGTGTAC
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99.2%;
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APPLICANT: Linsley, Peter
APPLICANT: Man Man
APPLICANT: Man Man
APPLICANT: Man Man
TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
FILLE REFERENCE: 9301-157-999
CURRENT APPLICATION UNMER: US/10/171,581
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/298,914
PRIOR APPLICATION NUMBER: 60/298,914
PRIOR FILING DATE: 2001-06-18
INMBER OF SEQ ID NOS: 366
SEQ ID NO 48
LENGTH: 1116
TYPE: DNA
ORGANISM: HOMO SEPIENS
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2001-06-18
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sequence 48, Application US/10171581
sequence 10, Application US/20030104426A1
publication No. US20030104426A1
GENERAL INFORMATION:
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Best Local 9
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778 AAGGTGATCTAA 789
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                                                                                                                                                    AGCAGATCTTCCTGGGGGCGTGGACAGCACACCACTTCTGGAGGTACTTTGCGGGC
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    TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA
                                     TTTGCCAGAACCCGCCTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGA 465
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ilarity 99.2%;
Conservative (
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Pred. No. 7.9e-194; 
0; Mismatches 3; Indels 3;
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                                                                                                                                           APPLICANT: MORTICK, Donna
APPLICANT: Hontson, Kory
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Clastle, Arthur
APPLICANT: Clastle, Arthur
APPLICANT: Clastle, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/22,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/22,880
PRIOR APPLICATION NUMBER: US 60/29,029
PRIOR APPLICATION NUMBER: US 60/29,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/29,336
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/29,336
PRIOR FILING DATE: 2001-05-9
PRIOR APPLICATION NUMBER: US 60/29,336
PRIOR APPLICATION NUMBER: US 60/29,345
PRIOR APPLICATION NUMBER: US 60/29,457
PRIOR APPLICATION NUMBER: US 60/29,457
PRIOR APPLICATION NUMBER: US 60/29,457
PRIOR APPLICATION NUMBER: US 60/29,884
PRIOR APPLICATION NUMBER: US 60/30,459
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US-09-917-800A-1327
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                                       SOFTWARE: PatentIn
SEQ ID NO 1327
LENGTH: 1196
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                                                                                             PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
ORGANISM: Rattus norvegicus
                                                                                                                                   APPLICATION NUMBER: US
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US-09-811-094-2

US-09-811-094-2

; Sequence 2, Application US/09811094

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; OTHER INFORMATION: Genbank Accession No. US-09-917-800A-1327
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                                                                                                  ATCTTCAGAGATGAGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG
                                                                                                                                         CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG
                                                                                                                                                                                                                                                                                                      TACTTCCCCACTCAAGCCCTCAACTTCGCCTTCAAGGATAAGTACAAGCAGATCTTCCTG
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                                                                         GGCATGGGGGGCGCCTTCGTGCTGCTGTACGACGAGCTCAAGAAGGTGATCTAA 897
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Pred. No. 1.1e-147;
0; Mismatches 188;
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APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Soumitra S.
APPLICANT: Scabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
ITITLE OF INVENTION: PRODUCTION OF ADENINE NU
ITITLE OF INVENTION: NOVEL ANT LIGANDS AND S
ITITLE OF INVENTION NUMBER: US/09/811,094
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 897
TYPE: DNA
ORGANISM: Homo saplen
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                                                                     CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC
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ACGGCCGTGGCCGGCGTGTCCTACCCCTTCGACACGGTGCGGCGGCGCGCATGATGATG
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                                                                                                           CTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCCTGTACCAAGGCTTTAACGTGTCT
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nilarity 78.9%;
Conservative
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2.8e-147;
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APPLICANT: Glevenger, William
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sout tw.
APPLICANT: Scabo, Tomas R.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Hoos, WALTER HOOS AND SCREENING ASSAYS THEREFOR TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE OF INVENTION NUMBER: US/09/810,644
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 37
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
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US-09-810-644-2
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Patent No. US20020012992A1
GENERAL INFORMATION:
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Best Local :
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eleen
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
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Similarity 78.9%;
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GGTGCCGCAGGGGCCACATCCCTGTGTTTTGTGTACCCTCTTGATTTTGCCCCGTACCCGT
                       GGTGCGGCCGGCCGACCTCCCTCTCGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC 420
                                                                                                             GGGGGCTGGACAAGCACACGCAGTTCTGGAGGTACTTTGCGGGCAACCTTGGCCTCCGGC 360
                                                                                        GGTGGTGTGGACAAGAGAACCCAGTTTTGGCGCTACTTTGCAGGGAATCTGGCATCGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sondra Eileen
APPLICANT: Wiley, Sondra R.
APPLICANT: Sabo, Tomas R.
APPLICANT: Schosh, Soumitra S.
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT PILING NUMBER: U$/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 897
TYPE: DNA
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     121 GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC 180
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                                              61 ATCTCCAAGACGGCCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGCTGCAGGTCCAGCAC 120
                                                                                                                                    1 ATGACAGATGCCGCATTGTCCTTCGCCAAGGACTTCCTGGCAGGTGGAGTGGCCGCAGCC 60
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78.98;
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RESULT 13

US-10-198-846-13437

Sequence 13437, Application US/10198846

Publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James
APPLICANT: Wang, Youzhen

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen
APPLICANT: Steinmann, Kathleen
APPLICANT: Wang, Youzhen

ITITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT APPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

INUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastEEQ for Windows Version 4.0

SEQ ID NO 13437

LENGTH: 1711
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2, 1397, 1398, 1399, 1400, 140
LOCATION: 1416, 1417, 1418, 1419, 1420, 144;
LOCATION: 1426, 1427, 1428, 1429, 1430, 144;
LOCATION: 1426, 1427, 1428, 1429, 1430, 144;
OTHER INFORMATION: n - A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1435, 1436, 1437, 1438, 1439, 1
LOCATION: 1445, 1446, 1447, 1448, 1449, 1
GOTHER INFORMATION: n - A,T,C or G
US-10-198-846-13437

64.98; Score 581
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                   CAGTCCGGGCGCAAAGGAGCTGACATCATGTACACGGGCACCGTCGACTGTTGGAGGAAG
                                                                                             ATGCTCCCCGACCCCAAGAACACGCACATCGTGGTGAGCTGGATGATCGCGCAGACCGTG
                                                                                                                                 CTGGCAGCGGACGTGGGAAAGTCAGGCACAGAGCGCGAGGTTCCGAGGCCTGGGAGACTGC
                                                                                                                                                                                                                                                           GGTGCGGCCGGCCGACCTCCCTCTGCTTCGTGTACCCCGCTGGATTTTTGCCAGAACCCGC
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                                                         CTGGTGAAGATCACCAAGTCCGACGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCCC
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  ATCTTCAGAGATGAGGGGGGCAAGGCCTTCTTCAAGGGTGCGTGGTCCAACGTCCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.9%;
nilarity 78.0%;
Conservative
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Pred. No. 7.1e-
0; Mismatches
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Sequence 1, Application US/09811094

Patent No. US20010044144A1

GENERAL INFORMATION:

APPLICANT: Davis, Robert E.

APPLICANT: Davis, Robert E.

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Wiley, Sounitra S.

APPLICANT: Wiley, Sounitra S.

APPLICANT: Hoosh, Monday S.

APPLICANT: Hoosh, Monday S.

APPLICANT: Hoosh, Monday S.

APPLICANT: Hoosh, Monday S.

APPLICANT: Hoo
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US-09-811-094-1
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Best Local :
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al Similarity 77.6%;
696; Conservative
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                                   CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAGGGCTTCAGTGTCTCC 540
                                                                                           TTGGCTGCTGATGTGGGCAGG----CGCGCCCAGCGTGAGTTCCATGGTCTGGGCGACTGT 477
                                                                                                                                                    CTGGCAGCGGACGTGGGAAAAGTCAGGCACAGAGCGCGAGGTTCCGAGGCCTGGGAGACTGC 480
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                                                                                                                                                                                                                                                   GGTGCGGCCGGCGGACCTCCCTCTGCTTCGTGTACCCGCTGGATTTTGCCAGAACCCGC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCCCAAGGAGCAGGGCGTGCTGCTCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC 240
; Score 564.2; DB 9; Length 9; Pred. No. 2.9e-139; O; Mismatches 198; Indels
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US-09-810-644-1
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-644-1
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
APPLICANT: Wiley, Robert E.
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soundtra S.
APPLICANT: MOOS, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088 42003
CURRENT APPLICATION NUMBER: US/09/810,644
RUMBER OF SED IT NOCE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 1, Application US/09810644
Patent No. US20020012992A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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              181 ATCCCTAAGGAGCAGGGCTTCCTCCTCTGGAGGGGTAACCTGGCCAACGTGATCCGT 240
                                                                                                                                  121 GCCAGCAAGCAGATCGCCGCCGACAAGCAGTACAAGGGCATCGTGGACTGCATTGTCCGC 180
                                                                   181 ATCCCCAAGGAGCAGGGCGTGCTGTCCTTCTGGAGGGGCAACCTTGCCAACGTCATTCGC 240
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Search completed: August 24, 2003, 05:40:58 Job time: 256 secs

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Maximum Match
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length: 2000000000
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1: /SIDS1/gcgdata/gei
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Copyright (c) 1993 - 2003 Compuq
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742.5	742.5	742.5	742.5	742.5	742.5	742.5	742.5	742.5	742.5	742.5	742.5	742.5	742.5	742.5	743	749.5	763	763	788.5	879.5	981	1044	1119	1119	1137.5	1254.5	1254.5	1288	1367.5	1385.5	1385.5	1385.5	1406	1412	1418
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1027	1009	992	381	381	381	381	363	363	363	363	346	346	346	346	379	386	484	484	301	298	222	228	315	315	307	299	299	263	325	297	297	297	293	298	429
21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	24	22	22	22	23	22	23	23	23	22	22	22	22	22	22	23	22	21	22	19	24
AAG38670	AAG38671	AAG38672	AAG38458	AAG37262	AAG37259	AAG36575	AAG38459	AAG37263	AAG37260	AAG36576	AAG38460	AAG37264	AAG37261	AAG36577	ABP81267	AAM00106	ABG27055	ABG15422	ABP73357	ABG18922	ABP74106	ABP43205	AAE21175	ABU53218	ABB58380	ABB67300	ABB66082	ABG27056	ABG15423	AAU10378	AAU01198	AAY71031	ABU53219	AAW61169	ABR41715
Arabidopsis thalia	Arabidopsis thalia		-						Arabidopsis thalia						Arabidopsis thalia	ATP carı	1 human	Novel human diagno	ida albi	human diag	TRICH SEQ 1	ovarian a	TRICH-19 pr	Human metabolism-a	Drosophila melanog	Drosophila melanog	ophila m	_		adenine		adenine nuc	metabolis	protein	Human DITHP organe

ALIGNMENTS

AAY71033 standard; Protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytostatlo; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; alzhelmer's disease; Parkinson's disease; Huntington's disease; dystonia; Alzhetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                   03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                               11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adenine nucleotide translocator ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-2000 (first entry)
                                                                                                                                                                                                                        03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200026370-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                         98US-0185904.
99US-0393441.
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Human

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RESULT 2
AAM39641
ID AAM:
XX AAM:
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DT 22-C
DT 22-C
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Hume
KW Hume
KW peri
KW alzi
KW amyce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                        Human polypeptide SEQ ID NO 2786.
                                                                                                                                                                                                                                  AAM39641 standard; Protein;
                                                                                                                                                 22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 46; Page 173-174; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
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DB; AAD00521.
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                                                                                                                                                                                                                                                                                                                                 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                   VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1543; DB 21; 100.0%; Pred. No. 4.6e-157; tive 0; Mismatches 0;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAI88642-AAI42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 2786; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442253/47.
N-PSDB; AAI58797.
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Zhou P,
                                                                                               VGIIIYRAAYEGYYDTAKGMLDDKNHHIVVSMIAQTVTAVAGVYSYEDTVRRMM
VGIIIYRAYEGYYDTAKGMLDDKNHHIVVSMIAQTVTAVAGVYSYEDTVRRMM
VGGIIIYRAYEGVYDTAKGMLDDKNHHIVVSMIAQTVTAVAGVYSYEDTVRRMM
                                                                                                                                                                                     IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                   MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                      298 AA;
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; 2000US-0552317.
; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0652191.
; 2000US-0693036.
; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0;
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; Pred. No. 4.6e-157;
0; Mismatches 0;
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Yang Y,
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Zhang J;
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RESULT 3
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XX ADUD
XX ADUD
XX ADUD
XX ADUD
XX Huma
XX Huma
XX MITC
KW MITC
KW MITC
KW ALZH
XX AUZ
YX HOMC
XX AUZ
YX HOMC
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                                                                                                                                                                                                                                                                                                                                            The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (GP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability components of incorescent protein (GP) or a FLASH sequence). The components of liversecent protein (GP) or a frasky that alter components of diseases associated with altered mitochondrial function or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mitochondrial encephalopathy, lactic acidosis, stroke, schizophrenia, and desfore a concert and desfore and 
                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynuclectide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
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                                                                                                                                                                                                                                                          Sequence
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Velicelebi G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adenine nucleotide translocator-3 (ANT-3) protein.
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                                                                                                                                                                                                                                                                                                                             hyperproliferative
                                                                                                                                                 Local Similarity
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                                                                                                                298;
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MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                                                                          298
                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                      disorders e.g. cancer, and
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                                                                                                        Score 1543;
Pred. No. 4.6
0; Mismatches
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The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide ANT polypeptide. ANT cuseful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, is useful for identifying an agent that binds to an ANT polypeptide, preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating and from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel recombinant expression construct translocator polypeptides, comprises a nucleic acid encoding the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; adenine nucleotide translocator; ANT;
mitochondrial matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3;
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Y, Carroll AK;
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                                                                                                                                      21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 6358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM41427 standard; Protein; 323 AA.
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                                 N-PSDB; AAI60583
                                                                                                                (HYSE-) HYSEQ INC.
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181 VGGIIIYRAAYEGVYDTAKGMLPDFKNYHIVYSWMIAQTVTAVAGVVSYEEDTVERRMM 240
181 VGGIIIYRAAYEGVYDTAKGMLPDFKNYHIVVSWMIAQTVTAVAGVVSYEEDTVERRMM 240
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Wang Z,
Zhou P,
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llarity 100.0%;
Conservative (
                                                                   Asundi V, Chen R,
Wehrman T, Xu C,
Goodrich R, Drmar
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Pred. No. 4.6e-157;
                                                                    hen R, Ma Y,
Xu C, Xue AJ,
Drmanac RT;
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                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Zhang J;
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

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PR 112
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                         Human; insulin receptor signaling; insulin receptor signaling modifier; ISM; diabetes; metabolic syndrome; antidiabetic.
                                                                                                                                                                                                                                                                                             Human insulin receptor signaling modifier SEQ ID NO:
                                                                                                                                                                                                                                                                                                                             11-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                             AA018516;
                                                                                                                                                                                                                                                                                                                                                                                                AAO18516 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 6358; 10078pp; English.
                                                                                                     11-JAN-2002;
                                                                                                                                       18-JUL-2002.
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Jte: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 265
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; 2001US-261226P.
; 2001US-261303P.
; 2001US-261304P.
; 2001US-261335P.
; 2001US-261336P.
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                                                                                                       2002WO-US01048
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                                                                                                                                                                                                                                                                                                                                                                                                  298
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12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
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12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method of identifying a candidate insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 160-161; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contacting an assay system comprising insulin receptor signaling modifiers with a test agent -
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                                                                                                                                            VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                         IPKEQGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                     QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                                                                                                                                    GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                                                                                          IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                  MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                             VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
                                                                      QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
                                                                                                                                                                                                                                                                                                                                                                                                                    298
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2001US-261456P.
2001US-261458P.
2001US-261459P.
2001US-261461P.
2001US-261518P.
2001US-261531P.
2001US-261532P.
2001US-261532P.
2001US-261590P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an insulin receptor signaling modulator, useful treating diabetes or metabolic disorders, compri-
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2001US-261695P.
2001US-261697P.
                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                     94.8%;
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                                                                                                                                                                                                                                                                                                                                                           13;
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Pred. No. 1.8e
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        DB 23;
L.8e-148;
hes 8;
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                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                      296
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AAY71032 standard; Protein;

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61

IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG

120 60

0

MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR

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(ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine cdi/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability ctransition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for crequiating mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore activity, for treating diseases associated with altered mitochondrial pore sociates, diabetes, dystonia, compating the properties and stroke (MELAS), hyperproliferative clasorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an accordance of the present sequence is an accordance of
                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD00520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              discloses a method to produce adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                         298
                                                                                                                                     Conservative
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99US-0393441
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                                                                                                                                                                    Score 1454;
Pred. No. 1
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1.7e-147;
hes 9;
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                                                                                                                                                                                                                298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dystonia;
                                                                                                                                Gaps
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RESULT 8
The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact vith other mitochondrial core components e.g. cyclophilins to regulate MFT. The present invention relates to a novel nucleic acid components of the protein construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MFT and/or cell survival. These agents are useful for the prevention or dysfunctional cell survival. Such as Albeimer's disease, diabetes compliants, Parkinson's disease, Huntington's disease, schizophrenia, continuous parking protein acidosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU01199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU01199 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy AN, Clevenger W,
Velicelebi G, Davis RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adenine nucleotide translocator-2 (ANT-2) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adenine nucleotide translocator-2; ANT-2; MTP; ondrial permeability translition pore component; ondrial core component; mitochondrial related d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bility transition pore component; cell survival, omponent; mitochondrial related disorder; cancer; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wiley SE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andreyev AY,
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                                                                                                                                                                                                                                                                                                                                 Anderson CM, Davis
Ghosh SS, Moos WH,
                                                                                                                                                                                                                                                                          WPI; 2002-055598/07.
N-PSDB; AAS16689.
                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-2001; 2001WO-US15416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial matrix protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10379;
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                                                                                                                                                                                                                                                                                                                                                                                           (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                   Davis
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hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                    181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                           121 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                              121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                    QSGRKGADIMYTGTVDCWRKIFRDEGGRAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                    VQGIIIYRAAYEGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMMM
                                                                                                                                                                                                               QSGRKGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEIKK
                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                              Score 1454; DB 22;
Pred. No. 1.7e-147;
                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                           180
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298
B
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Human adenine nucleotide translocator 2 (ANT2).

adenine nucleotide translocator;

RE, Clevenger W, W Pei Y, Carroll AK; Wiley SE, Miller WS, Szabo

Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide

Claim 44; Fig 2; 147pp; English.

The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nuclaic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or enkaryotic host cell a culturing the host cell. (I) is also useful for targeting a polypeptide a polypeptide

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RESULT 10
ABR41715
ID ABR41715
AC ABR41
XX NAR41
XX NAR41
AC ABR41
XX NAR41
AC ABR41
XX NAR4
AC ABR41
AC A
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Best Loc
Matches
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28-MAR-2001;
29-MAR-2001;
29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; dithp; diagnostic and therapeutic polynucleotide; diagnocancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic neurological disorder; gastrointestinal disorder; transport disconnective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal disease model; toxicological testing; transcript imaging;
                                                                                                                                                                                                                                                                                       05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            organelle-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR41715
                                                                                                                                                                                                                                       27-MAR-2002;
                                                                                                                                                                                                                                                                                                                                           WO200297031-A2
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Similarity 92.68;
74; Conservative ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQGIIIYRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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2001US-279619P.
2001US-280067P.
2001US-291080P.
2001US-29180P.
2001US-291829P.
2001US-291849P.
2001US-299428P.
2001US-299776P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
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Pred. No. 1.7e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
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1.7e-147;
hes 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis;
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Dufour ... Dam
Daughtery SC, Dam
David
                                                                                                                                                                                                 Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polyencoded by human diagnostic and therapeutic polynucleotide, induce antibodies -
                                                                                                                                                                                                                             N-PSDB; ACC46652
                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                           20-JUN-2001; 2001US-300001P
                                                                                                                                                                                                                                   2003-129518/12.
                                                                                                                                                                                                                                                              GE,
                                                                                                                                                                                                                                                                                INCYTE GENOMICS
                                                                                                                                                                                                                                                               Jones AL,
, Hillman
                                                                                                                                                                                                                                             Dam TC,
David MH,
cwaha R,
                                                                                                                                                                                                                                                            'n,
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                                                                                                                                                                                                                                                        Yu JY,
Liu TF,
                                                                                                                                                                                                                                                   Lewis
                                                                                                                                                                                                                                               P
                                                                                                                                                                                                                                                                     AB,
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                                                                                                                                                                                                                                               Lan RY,
                                                                                                                                                                                                                                                   Dahl CR,
I Tuason
Nguyen
SA, Chen
                                                                                                                                                                                                                                                   , Gietzen D, C
n O, Yap PE, A
n DA, Kleefeld
n AJ, Panzer SR
                                                                                                                                                                                                                                               Urashka
                                                                                                                                                                                                                 useful for
                                                                                                                                                                                                                                                    SR,
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Claim 27; SEQ

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No 1250;

591pp; English.

CC proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of for compounds which specifically bind a DITHP protein; and methods of CC assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins may be used in the CC diagnosis of a wide variety of conditions including cancer and other cell CC proliferative disorders; autoimmune or inflammatory disorders; bacterial, CC viral, fungal or parasitic infections; hormonal disorders; metabolic CC disorders; neurological disorders; gastrointestinal disorders; transport CC screen for modulators of protein activity or gene expression. DITHP CC proteins can additionally be used in analysis of the proteome of a tissue CC rell type and to induce antibodies. The dithp nucleic acids are CC additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in human disease or knock in the present sequence represents a DITHP protein which is an organelle-cassociated protein. The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (Acc46080-Acc46749) and to their encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP associated protein.

Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences. part of the directly from trom WIPO

Sequence 429 A

Query Match Best Local

Similarity

91.9%; 95.2%;

2e-143;

DB

Length

429;

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Matches
                                 181
                                                                  146
                                                                                                    121
                                                                                                                                     86
                                                                                                                                                                     61
                                                                                                                                                                                                      26
                                                                                  GAAGATSLCFVYPLDFARTKLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                        MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
               VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                     IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                     MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                    IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                      Score 1418; D
Pred. No. 2e-1
3; Mismatches
                                                                                                                                                                                                                                                                      ω
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                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                      6;
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                  180
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                                                                                                                                                                     120
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RESULT 11
AAW61169
ID AAW61
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                                                                                                                                                     Query Match
Best Local
                                                                                                                                      Matches
                                                                                                                                                                                                                                                 The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Tag dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, latcic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of ANTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or gene therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antl; Adenine nucleotide translocator; cloning; screening; DNA Taq dideoxy terminator cycle sequencing; oxidative phosphorylation; probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; lactic acidosis; degenerative muscle disease.
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 39-40; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graham BC, Macgregor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYEM-) UNIV EMORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-1997;
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                                                                                                                                                                                                                                         independent of ANT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1998-286608/25.
DB; AAV36479.
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  61
                            61
                                                                   H
                                                                                                                                                       Similarity
                                                                                   MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDXYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSGRKGADIMYTGTYDCWRKIFRDEGGKAFFKGA-W----SWYLRRMGGA 285
                                                               MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                                                                                                                                                                                        298 AA;
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0030017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US19882.
                                                                                                                                    91.5%; Score 1412; DB 19;
88.6%; Pred. No. 5.4e-143;
ive 19; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wallace
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A
                                                                                                                                    Indels
                                                                                                                                                                   Length 298;
                                                                                                                                    0;
                                                                                                                                  Gaps
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δÃ 밁 Q

1 ALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE

AISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKE 64

QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAG QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG

124 60

120

Query Match Best Local S Matches 263

Similarity

91.1%; 90.1%; 17;

Score 1406; DB 22; Pred. No. 2.3e-142; 7; Mismatches 12;

Indels Length 293;

0

Gaps

Conservative

G

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61

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RESULT 12
ABU53212
XX ABU533
XX ABU53
XX Human
XX Human
XX Human
XX Homo
XX Ho
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                                                                      This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-327840/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU53219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU53219 standard;
         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example III; Page 850; 1095pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEHU-) GERMAN HUMAN GENOME PROJECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-2000; 2000WO-IB01496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200112659-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene therapy; vaccine; disease treatment; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human metabolism-associated DKFZphtes3_35n12 homologue #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRWWW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0149499
99US-0156503
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RESULT 13
AAY71031
ID AAY71031
XX AAY71
XX AAY71
XX AAY71
XX AAY71
XX AAY71
XX Human
XX Human
XX Human
XX Human
XX Alaha
KW Alaha
KW Alaha
KW Mitco
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                     The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, leber's hereditary optic neuropathy, schizophrenia, mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystudiabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant construct encoding adenine polypeptide, useful e.g. in screening f against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; A adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; c mitochondrial permeability transition; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myoclonic epilepsy red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiParkinsonian; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71031 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-365619/31.
)B; AAD00519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKK 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis
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99US-0393441
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         lactic
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                                                                                                                                                                                                                                                                                                                                                                                                                                     175pp; English
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      acidosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξ
      stroke
schizophrenia, mitochondrial
stroke (MELAS), hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotide translocator for potential therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroleptic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IR;
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Best Local
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                                                                                                      WPI; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, mitochondrial diabetes and deafness (MIDD), an epilepsy red ragged fibre syndrome. The present sequence adenine nucleotide translocator ANT1 from human brain.
                                                                                                                                                                                                                                                                                          mitochondrial permeability transition pore component; cell sumitochondrial core component; mitochondrial related disorder; Alzheimer's disease; diabetes mellitus; hyperproliferative dis
                                                  New nucleic acid expression constructs, useful for screening for act that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                               Disclosure;
                                                                                                                                     Murphy AN,
Velicelebi
                                                                                                                                                                                         03-NOV-1999;
                                                                                                                                                                                                            03-NOV-2000; 2000WO-US30535
                                                                                                                                                                                                                                 10-MAY-2001
                                                                                                                                                                                                                                                      WO200132876-A2
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Human
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                                                                                                                                                                    (MITO-) MITOKOR.
                                                                                                      2001-291054/30
DB; AAS05901.
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                                                                                                                                                                                                                                                                                                                                                 adenine nucleotide translocator-1 (ANT-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                             adenine nucleotide translocator-1; ANT-1; MTP;
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                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                               Fig
                                                                                                                                                Clevenger
                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                     Davis
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                               <u>ب</u>
                              186pp; English.
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87.2%;
                                                                                                                                      RE;
                                                                                                                                                Wiley
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Pred.
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                                                                                                                                               Andreyev
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                                                                                                                                                ΑY,
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                                                                                                                                                Frigeri
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                                                                                                                                                                                                                                                                                                                   cell survival;
                                                                                                                                                                                                                                                                                                                            cyclophilin;
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                                                                                                                                                5
                                                                                 for agents
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The present (ANT-1) prot

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represents proteins a

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human adenine nucleotide tra re mitochondrial permeability

translocator-1

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AAUT0378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                         Anderson CM, Davis RE, Clevenger W, W
Ghosh SS, Moos WH, Pei Y, Carroll AK;
                                                                                                                                                                                                                                                                                                           11-MAY-2001; 2001WO-US15416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; adenine nucleotide translocator; ANT;
mitochondrial matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human adenine nucleotide translocator 1 (ANT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU10378 standard; Protein; 297
                                                                                                                                                                                                                                 11-MAY-2000; 2000US-0569327
                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200185944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                   (MITO-) MITOKOR.
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260; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGATSLCEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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Pred. No. 3.8e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                       Wiley SE,
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                                                                                            Miller SW,
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                                                                                                Szabo TR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid comprising a adenine nucleotide translocator (ANT) polypeptide. ANT CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT CC matrix for ADP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or enwaryotic host cell and CC culturing the host cell. (I) is also useful for rayeting a polypeptide of interest to a mitcohondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT CC ligand is useful for determining the presence of an ANT polypeptide. ANT CC ligand is useful for determining the presence of an ANT polypeptide. CC preferably ANT, ANT2 or ANT3 in a biological sample and for isolating covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for Identifying an agent that interacts with an ANT polypeptide. CC covalently bound to a solid phase. Detectably labeled ANT ligand is also cuseful for Identifying an agent that interacts with an ANT polypeptide. CC The present sequence represents the amino acid sequence of human ANT1.
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Best Local Sim
Matches 260;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 44; Fig 2; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-055598/07.
DB; AAS16688.
                                                                                                                                                                                        180 VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPFDTVRRRMMM 239
                                                                                                                        181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                             241 QSGRKGADIMYIGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                      1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                   MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.8%; Score 1385.5; DB 23; Length 297; Alarity 87.2%; Pred. No. 3.8e-140; Conservative 21; Mismatches 16; Indels 1;
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Search completed: August 18, 2003, 16:11:32 Job time : 85 secs

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Title:
Perfect score:
Sequence:
Minimum
                                                                                                                               Scoring table:
                                Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                 OM protein -
                                                                                                                                                                                                                                                                                                               protein search, using sw model
                                                                                                                             BLOSUM62
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1543
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                                                                                                                                                                                                                                                                             August 18, 2003,
                                                                      283308 seqs, 96168682 residues
                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                                                                                   16:09:02; Search time 42 Seconds (without alignments) 682.340 Million cell updates/sec
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

sing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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40.2			48.4	48.5	48.6		49.3	49.4	49.5	49.6	49.8					63.4	64.4	67.3	67.3	67.5	•	91.1	91.3	91.9	92.2	92.3	94.2	98.0	100.0	Query Match I
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ADP, ATP carrier pr	717	ATD Carrior	carrier	ADP, ATP carrier pr	carr	hypothetical prote	carrier	ADP, ATP carrier pr	tical pro	carrier		transloc	carrier		carrier	•				tical pro	carrier	carrier	carrier	carrier	carrier (carrier		ADP,ATP carrier pr	Description

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121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180

GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180

61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120

IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120

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363 344.5	368	370.5	372	381	383	520.5	681.5	734.5	737.5	739.5	742	742.5	743
23.5	23.8	24.0	24.1	24.7	24.8	33.7	44.2	47.6	47.8	47.9	48.1	48.1	48.2
348 332	475	415	358	352	325	327	298	379	309	386	382	385	379
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probable mitochond Ca-dependent solut	nypornericai prote peroxisomal Ca-dep	hypothetical prote	hypothetical prote	mitochondrial solu	hypothetical prote	ADP/ATP translocas	hypothetical prote	ADP, ATP carrier pr	٠	٠	٠	ADP, ATP carrier pr	ADP, ATP carrier pr

ALIGNMENTS

A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein #status predicted cMAT> F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3> R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;HILE: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: B28116 ₽ Ş A; Molecule type: mRNA
A; Residues: 36-104,'R',106,'A',109-298 <HOU>
A; Cross references: GB: 03592; NID: g339722; PIDN: AAA36750.1; PID: g339723
A; Experimental source: liver 1. Mol. Biol. 206, 261-280, 1989 A; TITIE: DNA sequences of two expressed nuclear genes for human A; Reference number: S03893; MUID:89236396; PMID:2541251 A; Accession: S03894 C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: \$03894, B28116
R;Cozens, A.L.; Runswick, M.J.; Walker, J.E. ADP,ATP carrier protein T3 - human N;Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP, A; Gene: GDB: ANT3; ANT3Y A;Molecule type: DNA A;Residues: 1-298 <COZ> ;Status: not Query Match Best Local Similarity Genetics: Matches 298; 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60 compared with conceptual translation 100.0%; Score 1543; DB 1; ilarity 100.0%; Pred. No. 6e-129; Conservative 0; Mismatches 0; Indels Length 298; mitochondrial ADP/ATP 0; Gaps 0

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N;Alternate names: mitochondrial ADP,ATP translocase 2
C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: A29132; C28116
R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga
     A;Molecule type: mRNA
A;Residues: 1-298 <BATY
A;Residues: 1-298 <BATY
A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
A;Holdsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are expressed at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-298 < POW>
A; Repeat protein protein protein protein repeat homology
C; Supperfamily: ADP, ATP carrier protein repeat homology <ACPS
E; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACPS
E; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACPS
E; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACPS>
                                                                                                                                                                                                                                                                     R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R. J. Biol. Chem. 262, 4355-4559, 1987
A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat A;Reference number: A29132; MUID:87166056; PMID:3031073
A;Accession: A29132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP,ATP carrier protein T2 - bovine (;Species: Bos primigenius taurus (cattle) (;Species: Bos primigenius taurus (cattle) (;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999 (;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999 (;Date: 03-Mar-1999 (;Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A43646; MUID: 89229093; PMID: 2540808
A; Accession: B43646
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Biochemiatew. 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP, ATP carrier protein T2 - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
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97.7%;
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          expressed at the mRNA level in
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C;Keywords: duplication; transmembrane protein homology <ACP1>

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;107-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Accession: C28116
A;Molecule type: mkN
A;Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A;CCOSS-Teferences: GB:J03591; NID:9339720; PIDN:AAA36749.1; PID:9339721
A;Experimental source: clone pHAT3
          B
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R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
Biochim. Biophys. Acta 1152, 192-196, 1993
B;Title: Isolation and characterization of cDNA clones and a genomic clone encoding r A;Reference number: 160173; MUID:9401016 pMID:8399300
A;Accession: I60173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adenine nucleotide translocator - rat
C;Species: Rattus norvegicus (Norvey rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
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A; Note: there may be some cc
C; Superfamily: ADP, ATP carri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-298 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
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                                                                                                                                                                                                                                                                Query Match
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                                                                                     1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
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1 MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
                                                                                                                                                                                                                   h 92.3%; Score 1424; DB 2; Similarity 89.6%; Pred. No. 2e-118;
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Pred. No. 4.5e-121;
3; Mismatches 9;
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 205-298 < BABS
R; Oettmeier, W.; Masson, K.; Kalinna, S.
Eur. J. Biochem. 227, 730-733, 1995
A; Title: [(3)H]7-azido-4-isopropylacridone la
A; Reference number: S69369; MOID:95172058; PM
A; Accession: S69369
A; Molecule type: protein
A; Residues: 49-63;154-168 < OET>
C;Comment: This protein is synthesized in the cytosol and transported into the m C;Complex: homodimer C;Complex: homodimer C;Function:

A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial AT A;Note: located in the inner mitochondrial membrane C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein; ADP,ATP carrier protein; ADP,ATP carrier protein; homodimer; methylated amino acid; F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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WMBO
ADP,ATP carrier protein T1 - bovine
N;Alternate names: ADP/ATP translocase
C;Species: Bos primigenius taurus (catt
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A;Residues: 208-298 (ARS>
A;Residues: 208-298 (ARS>
A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
R;Aquila, H; Misra, D; Eulitz, M; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A;Title: Complete amino acid sequence of the ADP/ATP carrier A;Reference number: A03181; MUID:82188267; PMID:7076130
A;Accession: A03181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: residue 52 may be methyllysine R; Babel, W.; Wachter, E.; Aquila, H.; Kling Biochim. Biophys. Acta 670, 176-180, 1981 A; Title: Amino acid sequence determination A; Reference number: A61343; MUID:82046808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: A;Reference number: A24822; MUID:86295775; PMID:3017341
A;Accession: A24822
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R;Rasmussen, U.B.; Wohlrab, H.
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A; Residues: 2-51'x',53-70','x',72-109','x',111-298
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PMID:7867632
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Best Local
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241
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              QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                      VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMMM 240
                                                                                                     GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFTGLGNCITKIFKSDGLRGLYQGFNVS 180
                                                                                                                   GAAGATSLCEVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                         MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
QSGRKGADIMYTGTVDCWRKIAKDEGPKAFFKGAWSNVLRGMGGAFVLVLYDEIKKFV
                                                   VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQTVTAVAGLVSYPFDTVRRRMM
                                                                                                                                                                                                                                                                        92.2%;
                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                         Score 1422; DB 1;
Pred. No. 3.1e-118;
                                                                                                                                                                                                                                                             Mismatches
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298
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-298 <LAP>
A; Cross-references: EMBL: X74510; NID: g402627; PIDN: CAA52616.1; P
C; Genetics:
A; Gene: ANC1
C; Superfamily: ADP, ATP carrier protein: ADP, ATP carrier protein
C; Keywords: duplication; transmembrane protein
C; Keywords: duplication; transmembrane protein
F; 5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F; 110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F; 207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S:
A; Accession: S37210
A; Status: preliminary
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$37210
ADP,ATP carrier protein T1
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| :||:|| |||||||||||:||:||
WGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                             IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMM
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S37210
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Pred. No. 6
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A;Map position: 4q35-4q35
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-998/Product: ADP,ATP carrier protein #status predicted <MAT> F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1> F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Molecule type: mRNA
A;Residues: 1-15, A',17-146, 'RR',149,151-226, 'L',228-298 <NEC>
A;Residues: 1-15, A',17-146, 'RR',149,151-226, 'L',228-298 <NEC>
A;Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
A;Experimental source: clone pHAANT
R;Houldsworth, J; Attard; G.
R;Houldsworth, J; Attard; G.
R;Totle: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: A2816
A;Accession: A2816
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A;Residues: 1-298 <LIA>
A;Residues: 1-298 <LIA>
A;Residues: 1-298 <LIA>
A;Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659
A;Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659
A;Cosens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A;Reference number: S03893; MUID:89236396; PMID:2541251
A;Reference number: S03893; MUID:89236396; PMID:2541251
A;Reference number: S03893; MUID:89236396; PMID:2541251
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A;Residues: 1-298 <COZ>
A;Residues: 1-298 <COZ>
R;Neckelmann, N; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A;Title: CDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader A;Reference number: A39891; MUID:88041149; PMID:2823266
A;Accession: A39891
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N;Alternate names: mitochondrial ADP_ATP translocase 1

C;Species: Homo sapiens (man)

C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C;Accession: A44778; S03893; A39891; A28116

R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.

J. Biol. Chem. 264, 13998-14004, 1989

A;Title: A human muscle adenine nucleotide translocator gene has four exons, is located A;Reference number: A44778

A;Reference number: A44778

A;Accession: A44778
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A; Residues: 1-37 <HOU>
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Best Local :
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                                                                                121 GAAGATSLCFYYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263;
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                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                  IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%; Score 1409; DB 1; Length 298; 88.3%; Pred. No. 4.3e-117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Indels
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A;Cross=references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
E;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>
                                                                                                                                                                                                                                                                                                           ADP,ATP carrier protein - African malaria mosquito
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S31935; S31936
C;Baccession: S31935; S31936
R;Beard, C:B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A;Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
                                                                                                                                     A;Reference number: S31935
A;Accession: S31935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
A;Residues: 1-301 <BEA>
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A;Cross-references: EMBL:X70847
A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; transmembrane protein homology <ACP1>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A; Molecule type: mRNA
A; Residues: 1-298 <COS>
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N;Alternate names: adenine nucleotide translocase
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
C;Accession: $31814
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A; Accession: S31814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLWQVQTNDRTITADKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n 91.1%; Score 1405; DB 2; Similarity 89.2%; Pred. No. 9.8e-117; 34; Conservative 16; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQGIIIYRAAYFGVYDIAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laplace, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S31814
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240

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RESULT 10
T23207
T23207
r) Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z19707
A; Accession: T23207
A; Status.
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A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; A;Experimental source: clone K01H12
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-313 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; McMurray, A.
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F;209-300/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sin
Matches 231;
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                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                              LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY 187
                                                                                                                                                                                       LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS 127
                                                                                                                                                                                                                              VSVQGIIIYRAAYFGCFDTAKGMLPDPKNTSIFVSWAIAQVVTTASGIISYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRIPKEQGIGAFCGGNLANVIRYFPTQALNFAFKDVYKQVFLGGVDKNTQFWRYFLGNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRIPKEQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLA 118
                                                                      RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQSGRKG
                                                                                                                                                                        AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGGAAGATSLCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGIIGLYRGFN
             ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYLDELKKVI 298
-DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
                                                        RAAYFGMFDTAKMVFTADGKKLNFFAAWATAQVVTVGSGIISYPWDTVRRRMMMQSGRK-
                                                                                                               LCFVYPLDFARTRLAADVGKA-NEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
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77.08;
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carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                    67.5%; Score 1041; DB 2; 70.9%; Pred. No. 1.7e-84;
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Pred. No. 3.6e-97;
23; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       December
                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                                                                                                  Length 313;
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313
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                                                                                                               203
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A; Dialus, Free: DNA
A; Molecule type: DNA
A; Residues: 1-300 <WIL>
A; Cross-references: EMBL: Z82059; PIDN: CAB04874.1; GSPDB: GN00021; CESP: T27E9.1
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T25371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T01B11.4 - Caenorhabditis elegans C;Specias: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C;Accession: T25850 R;Geisel, C.; Stellyes, L.
                                                                                                                                                                                                                                                                                     hypothetical protein T27E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t/C;Accession: T25371 R;Lloyd, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
A;Introns: 4/1; 191/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: The sequence
A; Reference number: Z20099
A; Accession: T25850
                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: Z20024 A; Accession: T25371 A; Status: preliminary; transport
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                                                                 A; Map position: 3
A; Introns: 20/1; 41/3;
C; Superfamily: ADP, ATP
                                                                                                                     A; Gene: CESP:T27E9.1
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A; Residues: 1-313 <GEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4
A;Experimental source: strain Bristol N2; clone T01B11
                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          263
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Similarity 70.9%;
07; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGRKG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                            115/2 carrier protein; ADP,ATP carrier protein repeat
                                                                                                                                                                                                                   translated
               67.38;
                                                                                                                                                                                                                                                                     Library,
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Score 1038; DB Pred. No. 3e-84; 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1039; DB 2;
Pred. No. 2.6e-84;
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                                                                                                                                                                                                                                                                       November 1996
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                                DB 2;
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                                  Length 300
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                                                                 homology
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Matches

Local

Similarity

Conservative

37;

49;

4;

Gaps

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R;Le, T.; Weinstock, L.; Rifkin, L.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid W02D3.
A;Reference number: 218308
A;Accession: 715206
A;Accession: 715206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-300 <LET>
A;Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AAB54179.1; GSPDB:GN
A;Experimental source: strain Bristol N2: clone W02D3
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: CESP:WUZD3.0
A;Map position:
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
F;9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>
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T15.206
hypothetical protein W02D3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #to
C;Date: 20-Sep-1999 #to
C;Date: 71.506
C;Accession: T15.206
C;Acce
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             RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 SGGAAGATSLCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFF 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ARVPKEQGYAAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA 118
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ADP,ATP carrier protein - Chlorella kessleri
C;Species: Chlorella kessleri
C;Species: Chlorella kessleri
C;Datc: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C;Accession: A41677
C;Accession: A41677
Biol. Chem. 266, 24044-24047, 1991
A;Title: Glucose increases the expression of the ATP/ADP translocator and the glycera
A;Reference number: A41677; MUID:92084708; PMID:1748677
A;Accession: A41677
A;Accession: A41677
A;Accession: A41677
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A;Molecule type: mRNA
A;Residues: 1-339 <HIL-
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E;184-235/Domain: ADP,ATP carrier protein repeat homology <ACCP2>
F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACCP3>
F;241-329/Domain: ADP,ATP carrier protein repeat homology <ACCP3>
                                                                                                                                                                                                                                                   ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum)
ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum)
N;Alternate names: ADP/ATP transporter
C;Species: plasmodium falciparum
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
C;Accession: 568993; 551132
C;Accession: 568993; 551132
Eur. J. Blochem. 228, 86-91, 1995
A;Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the human ma
A;Reference number: 568993; MUID:95188918; PMID:7883016
A;Accession: 568993; MUID:95188918; PMID:7883016
A;Accession: 568993; MUID:95188918; PMID:7883016
A;Accession: 568993; MUID:95188918; PMID:7883016
A;Accession: 568993; MUID:95188918; PMID:CAA5841.1; PID:9623335
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F;103-301/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;209-301/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;209-301/Domain: ADP,ATP carrier protein repeat homology <ACP1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 GATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
                                                                                                                            183;
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7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAAD--KQYKGIVDCIVRIPKE 64
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98; Conservative
                                                                                                                                                                Similarity
                                                                                                                       61.1%; Score 943; DB 2; Length 301; llarity 61.8%; Pred. No. 7.6e-76; Conservative 45; Mismatches 62; Indels
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Db 8 NFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPEIKSGQVERYSGLINCFKRVSKE 67 Oy 65 OGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124	Sear Job	문 5	망	QΥ	₽	Qy	DЪ	γO	ర్
8 NFAADFLMGGISAAISKTVVTDIERVKMLIQTQDSIPEIKSGQVERYSGLINCFKRVSKE 67 65 OGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGAAG 124	ch com								
NFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPEIKSGQVERYSGLINCFKRYSKE 67 OGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124	plet 43	246	186	185	127		88	65	œ
	ted: August 18, 2003, 16:14:34 secs	RKGKEEIQYKNTIDCWIKILRNEGFKGFFKGAWANVIRGAGGALVLVFYDELAKVI 298 RKGKEEIQYKNTIDCWIKILRNEGFKGFFKGAWANVIRGAGGALVLVFYDELAKVI 301	IVYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPFDTVRRMMMMSG 245	IIYRAAYEGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMMMQSG 243	AISLLIVYPLDFARTRLASDIGK-GKDRQFTGLFDCLAKIYKQTGLLSLYSGFGVSVTGI 185	ATSLCEVYPLDEARTRLAADVGKSGTEREERGLGDCLVKITKSDGIRGLYQGESVSVQGI 184	OGVLSLWRGNVANVIRYFPTQAFNFAFKDIFKNIF-PRYDQNTDFSKFFCVNILSGATAG 126	QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124	NFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPEIKSGQVERYSGLINCFKRVSKE 67

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Title:
Perfect score:
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1543
1 MTEQAISFAKDFLAGGIAAA.....LRGMGGAFVLVLYDELKKVI 298
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	2 1	Result
1463 1445 1442 1448 1418 1419 1204 1254.5 1708.5 778.5 778.5 7760.5 760.5 760.5 760.5 750.	1543 1512	Score
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678 1 CMC1_HUMAN 075746 322 1 GDC_RAT P16561 702 1 CMC1_CAEEL Q21153 325 1 UCP5_HUMAN 095258 326 1 UCP5_HOMAN P16260 325 1 UCP5_HOMAN 016260 326 1 YEOR SCHPO Q13805 675 1 CMC2_HUMAN Q91320 315 1 MFT_HUMAN Q91341 315 1 SA18_HUMAN Q91344 312 1 UCP3_HUMAN P55916 676 1 CMC2_MOUSE Q9qxx4
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EMBL; BC014775; AAH14775.1; -.
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MIM; 300151; -.
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PRINTS; PR00926; MATOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER
Mitochondrion; Inner membrane;
Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0005744; C:mitochondrial inner membrane translocase GO:0005471; F:ATP/ADP antiporter activity; NAS. GO:0006854; P:ATP/ADP exchange; TAS. erpro; IPR002067; Mit_uncoupling. erpro; IPR002030; Mit_uncoupling. erpro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane
181
                        181
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                                                                                                                                                                          Н
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adult human liver.";
tl<u>Acad. Sci. U.S.A.</u> 85:377-381(1988).
             VQGIIIYRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                           GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                                                                                                                 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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298 AA;
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ilarity 100.0%;
Conservative 0
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S -> F (IN REF. 3; AAH14775).
; 18534E9F0E49672F CRC64;
                                                                                                                                                                                                             Score 1543; DB 1;
Pred. No. 3.6e-128;
                                                                                                                                                                                                                                                                                                                          1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
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                                                                                                                                                                                                                          Length 298;
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01-JUL-1993 (Rel. 26, Last s
16-OCT-2001 (Rel. 40, Last a
ADP,ATP carrier protein, iso
nuclectide translocator 3) (
SLC25A6 OR ANT3
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ADT3_BOVIN
P32007;
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Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";
Biochemistry 28:866-873(1989).
-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; (
Mammalia; Eutheria;
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PIR; B43646; B43646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                            REPEAT
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                                                                                          119ene family.

NSMEM 12

NSMEM 13

NSMEM 117

NSMEM 117

NSMEM 214

NSMEM 273

EAT 12

EAT 209

GENCE 298 AA
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iPR002030; Mit_uncoupling.
iPR001993; Mitoch_carrier.
     Conservative
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26, Last sequence update)
40, Last annotation update)
rotein, isoform T2 (ADP/ATP ocator 3) (ANT 3).
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                                                                                                  32877 MW;
                        98.0%;
97.7%;
                                                                                                                                                                                                                                                                                                                                                            membrane;
     4.
                           Score 1512;
Pred. No. 1
                                                                                                                                                                                        1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
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        Mismatches
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        1.9e-125;
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                                                 Length 298;
        Indels
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P05141; 043350;
13-AUG-1987 (Rel. 05, Created)
01-OCT-1994 (Rel. 30, Last sequence upda
28-FEB-2003 (Rel. 41, Last annotation up
ADP,ATP carrier protein, fibroblast iso;
(Adenine nucleotide translocator 2) (AMS SEC25A5 OR ANT).
                                                                                                                                                                                                                                                                                                                                                                               TISSUE--lacenta;

MEDLINE-90375457; PubMed-2168878;

MEDLINE-90375457; PubMed-2168878;

Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga F

"The human fibroblast adenine nucleotide translocator cloning and sequence.";

cloning and sequence.";

J. Biol. Chem. 265:16060-16063(1990).
                                                                                                                                                                            Submitted [5]
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-87166056; PubMed-3031073;
MEDLINE-1 D. Ferrari S., Kaczmarek L.,
                                                                                                                                                                                                                                                                                            growth-regulated.*;
J. Biol. Chem. 262:4355-4358(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                      level
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           "Molecular cloning of a
growth-regulated.";
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                                                                                                                              Houldsworth J., Attardi G
                                                                                                                                         MEDLINE=88124845; PubMed=2829183;
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                                            o distinct genes for ADP/ATP translocase are el in adult human liver.";
c. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
FUNCTION: CATALYZES THE EXCHANGE OF ADP AND MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane prot
            DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carr
                                    inner membrane
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                                                                                                                                                                                                                                  , Su Y., Baybayan P., Siruno A., Naga
a R.A., Schlessinger D., Chen E.Y.;
(JUN-1996) to the EMBL/GenBank/DDBJ
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EMBL/GenBank/DDBJ
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           mitochondrial carrier
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n E.Y.;
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                                                                                ACROSS
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r gene. Molecular
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RESULT 4
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ID ADT2_RAT
AC Q09073;
DT 01-FEB-1995
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GO; GO:0015207; F:adenine transporter activity; TAS.
GO; GO:0006832; P:small molecule transport; TAS.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carrier.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCARRIER.
PRINTS; PR00784; MITOCH_CARRIER; 3.
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REPEAT
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hes 275;
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                                                                           VQGIIIYRAAYFGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                             GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                                                      IPKEQGYLSEWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASG
                                                                                                                                                                 GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
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Pred. No. 3.8e
L3; Mismatches
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                                                                                                                                                                                                                                                                                                                                          V -> L (IN REF. 2).
3 -> E (IN REF. 2).
R -> L (IN REF. 4 A).
V -> G (IN REF. 5).
F973C3AED92C49D3 (
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2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
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(Rel. 31, Created)

STANDARD;

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Best Local S
Matches 272
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STRAIR-Sprague Dawley; TISSUE-Liver;

STRAIR-Sprague Dawley; TISSUE-Liver;

MEDLINE-94002161; PubMed-8399300;

Shinohara Y., Kamida M., Yamazaki N., Terada H.;

Shinohara Y., Kamida M., Yamazaki N., Terada H.;

Shinohara Y., Kamida M., Yamazaki N., Terada H.;

Shinohara Y., Kamida M., Yamazaki N., Terada a genomic clone encoding rat mitochondrial adenine nucleotide translocator.";

Biochim. Biophys. Acta 1152:192-196(1993).

1- FUNCTION: CATALIZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

1- SUBBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
(Adenine nucleotide translocator 2) (ANT 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D12771; BAA02238.1; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP, ATP carrier
(Adenine nucleot
SLC25A5 OR ANT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -|- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-|- SIMILARITY: Belongs to the mitochondrial carrier family.

    -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00784; MTUNCOUPLING. PROSITE; PS00215; MITOCH_CARRIER;
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                                                                                                                                                                                   1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                 Similarity
                                                  GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                  IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                              MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                 GAAGATSLCFYYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
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73
117
176
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Pred. No. 4.3e-120;
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                  Mismatches
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MOUSE STANDARD; PRT; 298 AA.

ADT2_MOUSE STANDARD; PRT; 298 AA.

P51881; 061311;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase (Adenine nucleotide translocator 2) (ANT 2).
          EMBL; U27316; AAC52838.1; -- EMBL; U10404; AAA19009.1; -- EMBL; X70847; CAA50196.1; -- EMBL; AF240003; AAF64471.1; -- MGD; MGI:1353496; Slc25a5.
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLC25A5 OR ANT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-C57BL/6; TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                      Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.; "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."; Gene 254:57-66(2000).
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20432087; PubMed=10974536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Costet P., Laplace C.;
Submitted (FEB-1993) t
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Rapid evolution of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                       inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                         FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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pseudoautosomal genes and their mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cambridge,
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iPR002067; Mit_carrier

AAF64471.1; -.

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01-FEB-1994 (Rel. 28, Cree

01-FEB-1994 (Rel. 28, Last

16-OCT-2001 (Rel. 40, Last

ADP, ATP carrier protein, F

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                                                 STRAIN-Sprague-Dawley, and Wistar; TISSUE-Heart, and Liver; MEDLINE-94002161; PubMed-8399300; Shinohara Y., Kamida M., Yamazaki N., Terada H.; "Isolation and characterization of cDNA clones and a genomiencoding rat mitochondrial adenine nucleotide translocator. Biochim. Biochims. Acta 1152:192-196(1993).

-I-FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS MITOCHONDRIAL INNER MEMBRANE.

-I-SUBUNIT: Homodimer.
-I-SUBUNIT: Homodimer.
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PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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Multigene fami
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                   inner membrane.
TISSUE SPECIFICITY:
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                                                                                                                                                                                                                                                                                                                                               norvegicus (Rat).
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IPR001993; Mitoch_carrier
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   BRAIN
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91.6%;
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Last annotation update)
in, heart/skeletal muscle
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                   HEART,
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                   SKELETAL
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                   MUSCLE
                                                     protein. Mitochondrial
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Murinae; Rat
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Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;

Rodentia; Chordata;

Sciurognathi;

Craniata; Vertebrata; Euteleostomi;

isoform T1 (ANT 1)

l (ADP/ATP L) (mANC1).

Muridae;

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ADTI_MOUSE STANDARD; PRT; 298 AA.

PA8962; 062164;

PO1-FEB-1996 (Rel. 33, Created)

PO1-FEB-2003 (Rel. 41, Last sequence update)

PO1-SEP-2003 (Rel. 42, Last annotation update)

PO1-SEP-2003 (Rel. 42, Last sequence update)

PO1-SEP-2003 (Rel. 41, Last sequence update)

PO1-SEP-2003 (Rel. 42, Last sequence update)

PO1-SEP-2003 (Rel. 41, Last sequence update)

PO1-SEP-2003 (Rel. 42, Last sequence update)
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PRINTS; PR00784; MITOCH_CARRIER;
PROSITE; PS00215; MITOCH_CARRIER;
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EMBL; D12770; BAA02237.1;
PIR; I60173; I60173.
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an email to license@isb-sib.ch).
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; Mit_uncoupling.
; Mitoch_carrier.
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PIR; S37210; S37210

MGD; MG:1353495; Slc25a4.

InterPro; IPR0020507; Mit_carrier.

InterPro; IPR002030; Mit_uncoupling.

InterPro; IPR001993; Mitcoch_carrier.

Pfam; PF00155; Mitc_carr; 3.

PRINTS; PR00784; MITWOCH_CARRIER.

PRINTS; PR00784; MITWOCH_CARRIER; 3.
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SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-97059403; PubMed-8903724;
MEDLINE-97159403; Prancke U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
"Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Muscle;
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                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lapiace C., Costet P.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                 U27315; AAC52837.1; -.
X74510; CAA52616.1; -.
AF240002; AAF64470.1; -.
BC003791; AAH03791.1; -.
BC026925; AAH26925.1; -.
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ADT1_BOVIN
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P02722;
21-JUL-1986
01-JUL-1993
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MEDILINE-82188267; PubMed-7076130;
MEDILINE-82188267; PubMed-7076130;
Meguina H., Misra D., Eulitz M., Klingenberg M.;
"Complete amino acid sequence of the ADP/ATP carrie
mitochondria.";
Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
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Multigene fami
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (AD
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Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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"Two bowine genes for mitochondrial AD
differences in various tissues.";
Blochemistry 28:866-873(1989).
SEQUENCE OF 207-297 FROM N. A.
MEDLINE-86295775; PubMed-3017
Rasmussen U.B., Wohlrab H.;
"Bovine cardiac mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
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Wohlrab H.; mitochondrial ADP/ATP-carrier: two distinct mRNAs and
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                                                    PubMed-3017341;
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f the ADP/ATP carrier
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ADP/ATP translocase
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PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MIUNCOUPLING.
PROSITE; PS00215; MITOCH CARRIER;
Mitochondrion; Inner membrane; Rej
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Res. Commun. 138:850-857(1986)
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89.2%;
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Keceman N.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-88041149; PubMed-2823266;

MEDLINE-88041149; PubMed-2823266;

Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;

"CDNA sequence of a human skeletal muscle ADP/ATP translocator:

"CDNA sequence of a human skeletal muscle ADP/ATP translocator:

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J. Mol.
[2]
   Science
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01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
SLC25A4 OR ANT1.
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                                                                                                     Kaukonen J., Juselius J.K., Tiranti
Comi G.P., Keranen J., Peltonen L.,
                                                                                                                                                                                                                                                                                                                                Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are level in adult human liver.";
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Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
Pa human muscle adenine nucleotide translocator gene has four of the state 
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Mammalia; Eutheria;
                           "Role of adenine nucleotide translocator Science 289:782-785(2000).
                                                                                                                                                                                VARIANTS PEO PRO-114 AND MET-289.
MEDLINE=20385067; PubMed=10926541;
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EXCHANGE
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ADP

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Query Match
Best Local
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PRINTS; PRO0926; MITOCARRIER.
PRINTS; PRO0784; MITOCOPLING.
PROSITE; PS00215; MITOCH_CARRIE.
Mitochondrion; Inner membrane; 1
Multigene family: Nicco-
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EMBL; J03593; AAA36751.1; -.
EMBL; J04982; AAA51736.1; -.
EMBL; BC008664; AAH08664.1; -.
EMBL; BC008664; AAH08664.1; -.
PIR; A44778; A44778.
Genew; HGNC:10990; SLC25A4.
                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
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DISEASE: Defects in SLC2504 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.

SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0006832; P:small molecule transport; erPro; IPR002067; Mit_carrier. erPro; IPR002030; Mit_uncoupling. erPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005987; C:integral to plasma membrane; TAS. GO:0005739; C:mitochondrion; TAS. GO:0015207; F:adenine transporter activity; TAS. GO:0006091; P:energy pathways; TAS. GO:0000002; P:mitochondrial genome maintenance; TAS.
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SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
             61
                                                                                                                                                                                                                                                                  Similarity
                                   IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                               MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                  MGDHAWSFLKDFLAGGVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                                                                                                                                                                                                                16
147
227
298 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rane; Repeat; Transmembrane; Transport;
mutation.
                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          A -> P (IN PEO).

/FTId=VAR_012111.

V -> M (IN PEO).

/FTId=VAR_012112.

C -> A (IN REF. 3).

KGA -> RR (IN REF. 3).

V -> L (IN REF. 3).
                                                                                                                                                                                                                                                           Score 1409; DB 1;
Pred. No. 2.1e-116
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(POTENTIAL).
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., II. P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Hichards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Daster E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Broktein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Doung J., Mays A.D., Dev I., Dietz S.M.,
RA Gepalos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA Gepalos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA Douston K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyman C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyman C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyman C.,
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Q26365; 991614; Q26254; Q95530; Q9VZ/U;
Q26365; 991614; Q26254; Q95530; Q9VZ/U;
Q26365; P016; 1498 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
ADP, ATP carrier protein (ADP/ATP translocase) (Acenine nucleot translocator) (ANT) (Stress sensitive B protein).
SESB OR A/A-T OR CG16944.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroides; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Berkeley;
MEDLINE=20196006; PubMed=10731132;
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"A CDNA clone encoding the ADP/ATP translocase of Drosophila melanogaster shows a high degree of similarity with the mammalian ADP/ATP translocases.";
J. Mol. Evol. 35:44-50(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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"Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila.";
Experientia 50:749-762(1994).
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MEDLINE-94350065; PubMed-7520869;
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Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,

A Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

A Nelson D.R., Nelson K.S., Pan S., Pollard J., Puri V., Reese M.G.,

A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

A Palazzolo M., Pittman G.S., Pan S., Pollard J., Smith T.,

B Palazzolo M., Pittman G.S., Pan S., Pollard J., Smith T.,

B Palazzolo M., Pittman G.S., Pan S., Pollard J., Stopski M.P., Smith T.,

B Palazzolo M., Pittman G.S., Pan S., Pollard J., Stopski M.P., Smith T.,

B Palazzolo M., Pittman G.S., Pan S., Pollard J., Wang R., Smith T.,

B Palazzolo M., Pittman G.S., Pan S., Pollard J.,

B Shue B.C., Siden Kiamos I., Stopski M.P., Smith T.,

B Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

B Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

B Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

B Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

B Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

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B Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

B Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

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B Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

B Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weinstock G.M., Weinstock G.M., Weinstock G.M.,

B Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weinstock G.M.,
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EMBL; $71762; AAB31734.3; -.
EMBL; Y10618; CAA71628.1; -.
EMBL; AE003484; AAF47957.1; -.
EMBL; AE003484; AAF47957.1; -.
EMBL; AY070894; AAL48516.1; -.
EMBL; YANOTORE SEBLIC SEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some or send an email to license@isb-sib.ch).
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"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Berkeley: TISSUE-Larva, Ovary, and MEDILNE-22426066; PubMed-1257559; Stapleton M., Carlson J.W., Brokstein P., George R.A., Guarin H., Kronmiller B., Pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00926; MITOCARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kimmel B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane (By similarity).

DOMAIN: Composed of three homologous domains.

SIMILARITY: Belongs to the mitochondrial carrier family.
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SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
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Lei Y., Levitsky A.A., Li
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GI -> QV
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transport; IMP.
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C (IN REF. 2).
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J., Li Z.,
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01-NOV-1997
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Q27238;
TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@fisb-sib.ch).
           PROSITE; PS00215; MITOCH CARRIER; 3.

Mitochondrion; Inner membrane; Repeat; Transmembrane; TRANSMEM 14 31 (POTENTIAL).

TRANSMEM 75 93 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del> -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insect Mol. Biol. 3:35-40(1994).
-- FUNCTION: CATALYZES THE EXCHANGE OF MITOCHONDRIAL INNER MEMBRANE.
-- SUBUNIT: Homodimer (By similarity)
-- SUBCELLULAR LOCATION: Integral mem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gambiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gamblae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; In.
Neoptera; Endopterygota; Diptera; Nematocera
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last annotation update) ADP,ATP carrier protein (ADP/ATP translocase)
                                                                                                                                                      EMBL; L11618; AAB04104.1; -.
EMBL; L11617; AAB04105.1; -.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                 PRINTS;
                                                                                                                                        Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A cDNA encoding an ADP/ATP carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to
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                                                                                                                                    PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    С.В.,
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                                                                                                            PR00926; MITOCARRIER
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(Rel. 35, Last sequence up)
(Rel. 35, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crews-Oyen A.E., Kumar V.K.,
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er membrane;
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93 2
136 3
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in no way
commercial
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Best Local S
Matches 233
            EMBL, M/6669, AAA33027.1; -.
PIR; A41677; A41677.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr;
Pfam; PF00153; mito_carr;
PFRINTS; PR00926; MITOCARRIER.
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=92084708; PubMed=1748677;

Hilgarth C., Sauer N., Tanner W.;

"Glucose increases the expression of the ATP/ADP translocator and glyceraldehyde-3-phosphate dehydrogenase genes in Chiorella.";

J. Biol. Chem. 266:24044-24047(1991).

-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translocator) (ANT).
Chlorella kessleri.
Eukaryota; viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ADP_ATP_carrier_protein (ADP/ATP translocase)
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TRANSMEM
TRANSMEM
                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
   PROSITE;
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233; Conserv
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MITOCH_CARRIER;
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5 (POTENTIAL).
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TRANSMEM 4.1
TRANSMEM 10.0
TRANSMEM 15.
TRANSMEM 20.0
TRANSMEM 20.0
                                                                                                  Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
Submitted (AUG-1994) to the EMBL/GenBank/DDJ databases.
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADD AND ATD ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
-i- SUBURIT: HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
01-CCT-1994 (Rel. 30, Last annotation update)
ADP.ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ATT 3).
AAC3 OR YBR085W OR YBR0753.
                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288c;
Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,
Vissers S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                   SEQUENCE OF 38-307 FROM N.A. STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE-90324269; PubMed-2165073;
KOlarov J., Kolarova N., Nelson N.;
"A third ADP/ATP translocator gene in yeast.";
J. Biol. Chem. 265:12711-12716(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Inner membrane.

DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

SIMILARITY: Belongs to the mitochondrial carr
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277 ---GGEQYNGTIDCWRKVAQDEGMKAFFKGAWSNYLRGAGGAFYLVLYDEIKKFI 329
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Pfam; PF00153; mito_carr; 3.
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RESULT 15
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ID ADT_SCHPO
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DT 01-NOV-1997 (
DT 01-NOV-1997 (
DT 28-FEB-2003 (
DE ADP,ATP carri-
DE translocator)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure, evolution and expression translocator gene from Chlamydomonas Mol. Gen. Genet. 237:134-144(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S30259; S30259.
InterPro; IPR002067;
InterPro; IPR001993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 ADP, ATP carrier protein translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MO1. Gen. Genet. 237:134-144(1993).
-!- FUNCTION: CATALYZES THE EXCHANGE
MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBURIT: Homodimer.
SUBCELLULAR LOCATION: Integral
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                                                                                                                                         296 VIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                        RRMMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK
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                        (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation updat
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12 29 1
74 92 2
16 133 3
78 197 4
17 234 5
8 AA; 33528 MW;
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                                                                             STANDARD;
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                                                                                                                                                                                           -GSAVKYNSSFHCFQETVKNEGMKSLFKGAGANILRAVAGAGVLAGYDQLQ
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              (ADP/ATP translocase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                55;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 772; DB 1;
Pred. No. 1.7e-60;
5; Mismatches 81;
                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
D477CF0E72B7A53F
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                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Transport.
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               nucleotide
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RA Wood V. Gwilliam R. Rajandream M.A. Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Bakham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gentles S., Goble A., Hamiln N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamiln N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornaby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Mooney B., Moule S., Wangall K., Murphy L., Niblett D., Odeil C.,
RA Molory B., Moule S., Mangall K., Murphy L., Niblett D., Odeil C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Woestl D., Hilbert H.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Woore K., Hurst S.M.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galllardin C., Tallada v.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Galllardin C., Tallada v.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RI Mature 415:817-1880 (2002).
CC -- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Couzin N., Trezeguet V., Saux A.L., Lauquin G.J.M.;
"Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae.";
Gene 171:113-117(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-972;
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Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schlzosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schlzosaccharomycetes;
Schlzosaccharomycetales; Schlzosaccharomycetaceae;
                                                             GENEDB_SPOMDE; SPBC530.10c; ...
InterPro; IPR0012067; Mit_Carrier.
InterPro; IPR001293; Mitoch_carrier.
InterPro; IPR00133; mito_carr; 3.
PRINTS; PR00125; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21848401; PubMed-11859360;
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                                                                                                                                                                           EMBL; AL023634; CAA
PIR; T40526; T40526
GeneDB_SPombe; SPBC
                                                                                                                                                                                                                                                 EMBL; Z49974; CAA90275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane.

1. DOMAIN. COMPOSED OF THREE HOMOLOGOUS DOMAINS.

1. SIMILARITY: Belongs to the mitochondrial carrier family.
                Mitochondrion;
TRANSMEM 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
  Inner membrane; Repeat; Transmembrane; 8 48 1 (POTENTIAL).
3 111 2 (POTENTIAL).
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                                                   Transport.
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SEQUENCE
263 TSGEA---VKYSSSFECGRQILAKEGARSFFKGAGANILRGVAGAGVLSIYDQVQ 314
                                                                     182 OGIIIYRAAYEGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMMM 240
                                                                                                                124 GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV
                        241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                   203 VGIVVYRGLYFGMYDTLKPVVLVGPLEGNFLASFLLGWAVTTGSGVASYPLDTIRRRMM
                                                                                                   143 GAASLLFVYSLDYARTRLANDAKSAKKGGEROFNGLVDVYRKTYRSDGLRGLYRGFGPSV
                                                                                                                                                                              64
                                                                                                                                                                                                                      7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADK---QYKGIVDCIVRIPK 63
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                   TFFFDFMMGGVSAAVSKTAAAPIERVKLLIQNQ--DEMIRAGRLSHRYKGIGECFKRTAA
                                                                                                                                                                                                                                                                                                           131
197
222
289
322
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                         151 3
217 4
242 5
309 6
35020 MW;
                                                                                                                                                                                                                                                           49.8%; Score 769; DB 1; Length 322; 53.6%; Pred. No. 3.3e-60; tive 50; Mismatches 75; Indels 12;
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(POTENTIAL).
(POTENTIAL).
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                                                                                                       202
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search completed: August 18, 2003, 16:12:02
Job time : 25 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Query
Match
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
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sp_phage:*
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sp_unclassified:*
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sp_archeap:*
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sp_virus:*
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046373
3 Q919M3
9 Q919M9
1 Q8BVI9
1 Q9PRH2
2 Q9YIC4
Q9SYX4
4 Q91336
Q8IRAO
Q8IRAO
Q8IRAO
Q914404
Q91404
Q1404
Q25129
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                                                                                                                                                                                                                                                                                                                SUMMARIES
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O8aym3 gallus gall
O8sqh5 bos taurus
O8jhiO brachydanio
O46373 oryctolagus
O9j9m9 xenopus lae
O8bvi9 mus musculu
O9prh1 rana rugosa
O9yic4 rana rugosa
                                                                                                                                                                                                                                                                 Description
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
749	753	756.5	759	760	764	767.5	778.5	827	924	924	932	936	943	944	944	946.5	947	973.5	993	993.5	996	1036.5	1038	1039	1041	1119	1137.5	1159
48.5	48.8						50.5	•	•	٠	60.4	60.7	61.1	61.2	61.2	•	61.4	63.1	64.4	64.4		7.	67.3	67.3	•		73.7	75.1
315	307	306	303	307	326	302	305	170	308	306	308	305	301	301	301	307	301	318	300	300	309	310	300	313	313	315	307	254
ω	u	Ŋ	w	G	Ŋ	w	w	σ	G	u	رى د	σ	G	σ	σ	œ	υı	u	G	u	տ	10	G	Ç	Ŋ	4	v	11
083001	Q26697	Q18683	074260	076286	P91270	Q8J0M2	Q9P8M1	Q9XS69	Q8MVR6	Q8MVR5	Q8MVR8	Q8MVR7	Q26006	Q8MVR4	Q25692	Q9XM22	Q8IJ34	Q9ВJ36	017407	001813	097470	Q8H727	045865	P91410	Q21103	Q9H0C2	062526	Q8BKQ5
		caenorha	_	٠.	_	٠	Q9p8ml yarrowia li				æ		plasmodium	Q8mvr4 euplotes sp	<pre>2 plasmodi</pre>			Q9bj36 toxoplasma			097470 dictyosteli	Q8h727 phytophthor	O45865 caenorhabdi			Q9h0c2 homo sapien	062526 drosophila	Q8bkq5 mus musculu

ALIGNMENTS

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Q8SQH5;
Q1-JUN-2002
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adenine nucleotide translocator 2.
             OBJHIO;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Solute carrier family 25 member 5 protein.
SLC25A5.
SLC25A5.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IRR001993; mitoch_carrier. pfam; pr00155; mito_carr; 3. pr0521F; ps00215; miTrOCH_CARRIER; 3. SEQUENCE 298 AA; 32955 MW; CB689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamazaki N., Shinohara Y., Tanida K., Terada H., "Structural properties of mammalian mitochondrial ADP/ATP carriers: identification of possible amino acids that determine functional differences in its isoforms."; Mitochondrion 1:371-379(2002).
EMBL: ASU65433; BAB8673.1;
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Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                           Q8JHI0
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273; Conservative
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Danio.
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TISSUE-Skeletal muscle;

A Yamaguchi N., Kasal M.;

Tamaguchi N., Kasal M.;

Tegulates calcium release from sarcoplasmic reticulum of rabbit seletal muscle.";

J. Blochem. 335:541-547(1998).

1. J. Blochem. 335:541-547(1998).

2. -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

2. -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

3. REMBL, AB009365; BAA2377.1; --

3. REMBL, AB009365; BAA2377.1; --

3. RINTEPPO; IPRO02030; Mitch-Carrier.

3. InterPro; IPRO02030; Mitch-Carrier.

3. RINTERPOSS; PRO0926; MITOCARRIER.

3. RPINTS; PRO0926; MITOCARRIER.

3. RPINTS; PRO0784; MTUNCOUPLING.
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Matches 274; Conserv
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046373, 1998 (TIEMBLITEL 06, C.
01-UUN-1998 (TIEMBLITEL 23, L.
01-MAR-2003 (TIEMBLITEL 23, L.
ADP/AIP translocase, rashit
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InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; Mit_Locarr; 3.
PRINTS; PR00926; MITCCARRIER.
PRINTS; PR00784; MITCCH_CARRIER; 3.
PROSITE; PR00784; MITCCH_CARRIER; 3.
PROSITE; PR00784; MITCCH_CARRIER; 3.
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MEDLINE-22035902; PubMed-12006978;

MEDLINE-22035902; PubMed-12006978;

Method R.A., Sun Z., Antonelli M., Maldonado E., Chen W.,
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EMBL; AF506216; AAM34660.1;
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essential for early vertebrate development.";
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Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y.,
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryotolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryotolagus.
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Pred. No. 8
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P SEQUENCE FROM N.A., Khosrowshahian F., Varmuza S.L., Liversage R.A.

Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.

Texpensive M.J., Khosrowshahian F., Varmuza Emnit Specific Specific Specific Specific Specific Report Specific Mitchian F., Liversage R.A.

Replant PRO0193; Mitchian F., Varmuza Specific Mitchian F., Liversage R.A.

Replant PRO0193; Mitchian F., Varmuza S.L., Liversage R.A.

Replant PRO0193; Mitchian F., Varmuza B.L., Liversage R.A.

Replant PRO0193; Mitchian F., Varmuza B.L.

Replant Province Province P. Varmuza B.L.

Replant Province P. Varmuza B.
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01-CCT-2000 (TIEMBLI
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                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 23, Last annotation
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Pred. No. 1.3e
20; Mismatches
                                                                                                                                                                                                                                      Score 1421; E
Pred. No. 1.6e
L4; Mismatches
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.3e-120;
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..6e-120;
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; Pipidae;
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                             Q9PRH1 PRELIMINARY;
Q9PRH1;
Q9PRH1;
01-MAY-2000 (TrEMBLrel. 13, C)
01-MAY-2003 (TrEMBLrel. 13, I)
01-MAR-2003 (TrEMBLrel. 23, I)
ADP/ATP translocase.
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Q8BVI9;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
Solute carrier family 25.
                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome b
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK078077; BAC37117.1;
 Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; N
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Medulla oblongata;
MEDLINE-22354683; PubMed-12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                              VQGIIIYRAAYEGYYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM 240
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Rodentia;
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Last annotation update)
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                                        Last sequence update)
                                                           Created)
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Pred. No. 6.8e-120;
0; Mismatches 14;
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Sciurognathi;
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           Craniata;
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           Vertebrata;
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           Euteleostomi;
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annotation
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Neobatrachia;

Ranoidea;

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RESULT 8

QPPRIZ

ID QPPRIZ

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InterPro; IPR002067; Mit_Carrier.
InterPro; IPR002067; Mit_uncoupling.
Pfam; PF00153; Mito_Carr; 3.
Pfint; PF00153; Mito_Carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCHERIER; 3.
PROSTIE; PS00215; MITOCH_CARRIER; 3.
Membrane; Transpert.
Membrane; Transport.
Membrane; Transport.
SEQUENCE 298 AA; 33054 MM; B0E23AD56F548D36 CRC64;
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   SEQUENCE FROM N.A.

MEDLINE-99083429; PubMed-9866197;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

"The origin and differentiation of the heteromorphic sex chromosomes

"The origin and differentiation of the heteromorphic sex chromosomes

Z. W. X. and Y in the frog Rana rugosa, inferred from the sequences of

a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).

1-1-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL; AB008459; BAA36508.1; -.

EMBL; AB008459; BAA36509.1; -.
                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
ADP/ATP translocase.
Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Annura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9PRH2
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-8410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQGIIIYRAAYEGYYDTAKGMLFDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMM 240
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88.6%; Pred. No. 1.
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RESULT 9
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Best Local
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Best Local
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InterPro; IPR002067; Mit__carrier.
InterPro; IPR002030; Mit__ncoupling.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00926; MITOCAPLING.
PROSTIE; PS00784; MITOCH_CARRIER; 3.
PROSTIE; PS00215; MITOCH_CARRIER; 3.
Membrane; Transport.
Membrane; Transport.
SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia, Barrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9YIC4 PRELIMINARY; PRT; 298 AA.
Q9YIC4;
01-MAY-1999 (TIEMBLIFEL 10, Created)
01-MAY-1999 (TIEMBLIFEL 10, Last sequence update)
01-MAR-2003 (TIEMBLIFEL 23, Last annotation updat
ADP/ATP translocase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8410;
                                                                           Local Similarity es 262; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263;
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1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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88.3%; Pred. No. 3.6e-119;
tive 20; Mismatches 15;
                                                                                                90.9%;
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                                                                           Score 1402; DB 13;
Pred. No. 8.3e-119;
1; Mismatches 15;
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Ranidae; Rana.
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Best Local S
Matches 243
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Q95VX4;
Q95VX4;
Q1-DEC-2001 (TremBirel 19,
Q1-DEC-2001 (TremBirel 19,
Q1-MAR-2003 (TremBirel 23,
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF401758; AAL02100.1; -.
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   Q91336
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243; Conserv
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                                                                                                                                                                                                                       IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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   PRELIMINARY;
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81.5%;
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Last sequence update)
Last annotation updat
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Pred. No. 1.5e-109;
6; Mismatches 29;
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   PRT;
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scolopendridae;
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RESULT 12
Q81RA
Q81RA
AC Q81RA
DT 01-MA
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L Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
1 - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI.
2 - 1 - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI.
3 - 1 - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI.
4 EMBL; U44832; AAA97882.2;
6 InterPro; IPR001993; Mitoch_Carrier.
6 R InterPro; IPR002067; Mit_Carrier.
7 R Pfam; PF00153; mito_carr; 3.
8 PRINTS; PR00926; MITOCH_CARRIER.
8 PROSITE; PS00215; MITOCH_CARRIER.
9 R PROSITE; PS00215; MITOCH_CARRIER.
9 Membrane; Transmembrane; Transport.
9 SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
                                                                                            Q8IRA0;
01-MAR-2003
01-MAR-2003
01-MAR-2003
CG16944-PC.
                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Eukaryota; Brachycera;
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cai Q., Greenway S.C., Storey K.B.; "Differential regulation of the mitochondrial in wood frogs under freezing stress."; Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; N
NCBI_TaxID=45438;
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01-NOV-1996 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana sylvatica (Wood frog).
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 SEQUENCE
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|QSGRKGAEIMYSGTIDCWKKIARDEGGRAFFR
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3 (TrEMBLrel.
3 (TrEMBLrel.
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Neobatrachia;
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Last sequence up
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Pred. No. 8.2e-106;
9; Mismatches 17;
                                                                                                          sequence up
                                                                                                                                                         312
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a; Ranoidea;
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                                                          Insecta;
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Ranidae; Rana
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lowis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hrandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hrandon R.C., Baytar E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aphayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,
RA Dodson K., Doup L.B., Donnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.B., Donnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeyama C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Muzny D.M., Nelson D.L.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Halliam S.M., Woldsey K., Stappson M., Skupski M.P., Smith T.,
RA Halliams S.M., Woldsey K., Stappson M., Skupski M.P., Smith T.,
RA Halliams S.M., Woldsey K.C., Wulliams S., Kupski M.P., Smith T.,
RA Halliams S.M., Woldsey K.C., Wulliams C., Zhong L.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhong L.,
RA Yeh R.F., Zhong
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Representation of the control o
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K
Misra S., Crosby M.A., Matthews J.S., Prochnik S.E., Smith C.D.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
*Annotation of Drosophila melanogaster genome.";
*Annotation of Drosophila melanogaster genome.";
*Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                        Adams M.D., Celniker
Submitted (MAR-2000)
SEQUENCE FROM N.A
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                      S.E., Gibbs R.A., Rubin G.M., Vent to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    Venter C.J.;
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QT 10-QC
DT 01-QC
DT 01-QC
DT 01-QC
CALLEL
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QC NeOpt
QC CALLE
QC NEOPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SS mal seeking;
STRAIN-SS mal seeking;
Chen Z., Fair J.A., Batterham P.;
Chen Z., Fair J.A., Batterham P.;
"A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AFELBS87; AAR93232.1;
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP/ATP translocase.
Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 ATSLCFVYPLDFARTRLAADTGKGG-QREFTGLGNCLTKIFKSDGIVGLYRGFGVSVQGI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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126 TSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGII 185
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                                                                                                                                     GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                   GFASYWRGNMANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFLGNLASGGAAGA
                                                                                                                                                                                                                                        LGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMIDCFVRIPKEQ 68
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300 AA; 33036 MW; 545
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(TrEMBLrel. 23, Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Created)
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7237;
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PROSITE; PS00215; MITOCH_CARRIER; 3.

Membrane; Repeat; Transmembrane; Transport.

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SEQUENCE 288 AA; 31725 MW; 052BOCC00504
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Genetica 0:0-0(1997)
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7241;
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SEQUENCE 288 AA;
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
205.5	205.5	205.5	205.5	211	222	226.5	226.5	226.5	226.5	226.5	226.5	227.5	232.5	232.5	243.5	244	244
13.3	13.3	13.3	13.3	13.7	14.4	14.7	14.7	14.7	14.7	14.7	14.7	14.7	15.1	15.1	15.8	15.8	15.8
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US-09-547-983-56	US-08-946-719A-56	US-09-210-681-56	US-08-807-861A-56	PCT-US94-09799-1	US-09-501-558-4	US-09-547-983-37	US-08-946-719A-37	US-09-210-681-37	US-08-470-868A-37	US-08-807-861A-37	US-08-518-878B-37	US-08-294-522B-36	US-09-234-613-12	US-08-933-750C-12	US-08-775-009-32	US-09-503-579-2	US-09-318-199-2
Sequence 56, Appl	Sequence 56, Appl	•	Sequence 56, Appl	Sequence 1, Appl1	Sequence 4, Appli	37,	37,	•	37,	Sequence 37, Appl	37,	•	Sequence 12, Appl	•	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli

ALIGNMENTS

; NUMBER OF SEQ ID NOS: 54 ; SOFTWARE: FASTSEQ for Windows Version 3.0 ; SEQ ID NO 49 ; LENGTH: 298 ; TYPE: PAT ; ORGANISM: Homo sapien US-09-434-354-49 RESULT 1 US-09-434-354-49 Best Loc Matches Sequence 49, Application Patent No. 6562563 GENERAL INFORMATION: Query Match APPLICANT: Murphy, Anne N. APPLICANT: Clevenger, William APPLICANT: Wiley, Sandra Eileen APPLICANT: Wiley, Sandra Eileen APPLICANT: Holeyev, Alexander Y. APPLICANT: Frigeri, Luciano G. APPLICANT: Velicelebi, Gonul APPLICANT: Davis, Robert E. APPLICANT: Davis, Robert E. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS FILE REFERENCE: 660088.433 CURRENT APPLICATION NUMBER: US/09/434,354 CURRENT FILING DATE: 1999-11-03 Local Similarity nes 298; Conserv Conservative 100.0%; Score 1543; DB 4; 100.0%; Pred. No. 4.5e-166; Live 0; Mismatches 0; US/09434354 Length 298; 0 AND FOR Gaps

181 181 121 121

GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS

GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS

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1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR

MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR

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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298

QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298

VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240

VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM

240

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APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Walley, Sandra Elleen
APPLICANT: Frigeri, Luciano G.
APPLICANT: Prigeri, Luciano G.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: INTERACTIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660068.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 48
SEQ ID NO 48
LENGTH: 298
                                                                                               Patent No. 6013858

GENERAL INFORMATION:

APPLICANT: Wallace, Douglas C.

APPLICANT: Wallace, Douglas C.

APPLICANT: Wallace, Douglas C.

APPLICANT: MacGregor, Grant R.

TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine

TITLE OF INVENTION: Nucleotide Translocator Protein and Me

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

COTY: Boulder
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-48
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US-08-961-871-10
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Best Local Similarity 92.6
Matches 274; Conservative
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                                                                                                                                                                                                                                                                                                                  Sequence 10,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                     COUNTRY:
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6013858
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                                                                                     Colorado
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; MOLECULE TYPE: protein US-08-961-871-10
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APPLICATION NUMBER: US 60/030
PILING DATE: 01-NOV-1996
APTORNEY/AGRET INFORMATION:
NAME: FEIDET, DONNA M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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FILING DATE: 31-0CT-1997
CLASSIFICATION B00
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
264;
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                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                        91.5%; Score 1412; DB 3; Length 29
88.6%; Pred. No. 2.9e-151;
tive 19; Mismatches 15; Indels
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WS-09-43-354-47

(Sequence 47, Application US/09434354)

Patent No. 6562563

GENERAL INFORMATION:
APPLICANT: MUIPDY, Anne N.
APPLICANT: MILEY, Sandra Elleen
APPLICANT: MILEY, Sandra Elleen
APPLICANT: Hiley, Sandra Elleen
APPLICANT: Velicelebi, Gonnl
APPLICANT: Velicelebi, Gonnl
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: DAVIS, 1999-11-03

CURRENT FILING DATE: 1999-11-03

RUMBER OF SEQ ID NOS: 54

SOFTMARE: FASTSEQ for Mindows Version 3.0

SEQ ID NO 47

LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien

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US-09-996-243-289
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CURRENT APPLICATION NUMBER: US/09/96,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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Best Local Similarity 87.2
260; Conservative
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                                                                                                                                                                                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C13
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APPLICANT:
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Baker, Kevin P.
Botstein, David
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                                                                                                                                                                                                                                                                                        Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fong, Sherman
Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                   Paoni, Nicholas F.
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87.2%;
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R FILING DATE: 1998-05
R APPLICATION NUMBER: 6
R FILING DATE: 1998-06
R APPLICATION NUMBER: 6
        FILING DATE: 1998-00-1
: APPLICATION NUMBER: 60
                                                                          APPLICATION NUMBER: 60/
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE: 1998-06
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-05
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/1
FILING DATE: 1998-04-28
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FILING DATE: 1998-06-16
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                                       APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908

FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19

APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18

FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17

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US-09-188-930-339
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SOFTWARE: FRANKSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-339
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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Best Local
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Patent No.
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Best Local S
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
ITILE OF INVENTION: Compositions Isolated From Skin Cells
ITILE OF INVENTION: Compositions For Their Use
ITILE OF INVENTION NUMBER: US/09/188,930A
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFV-LVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 IDLAVYETLKNAWLOHYAVNSADPG----VFVLLACGTMSSTCGQLASYPLALVRTRMQA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 FVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRA 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 AYFGVYDTAKGM-----LPDPKNTHIVVSWMIAQTVTAVAG-VVSYPFDTVRRRMM 240
242 LWRGNGINVLKIAPESAIKFMAYEQMKR--LVGSDQET---LRIHERLVAGSLAGAIAQS 296
                                                                                                                                                              10 KDELAGGIAAAISKTAVAPIERVKILLQVQHASKQIAADKQYKGIVDCIVRIPKEQGVLS 69

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188 RHLVAGGGAGAVSRTCTAPLDRLKVLMQV-HASR----SNNMCIVGGFTQMIREGGAKS 241
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o. 6150502
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                                                                                                                                                                                                                                                              20.2%; Score 311; DB 3; Length 469; 29.4%; Pred. No. 1.7e-26; tive 62; Mismatches 111; Indels
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PRIOR EPILICATION NUMBER: 60/08948
PRIOR APPLICATION NUMBER: 60/089952
PRIOR APPLICATION NUMBER: 60/090246
PRIOR APPLICATION NUMBER: 60/090246
PRIOR APPLICATION NUMBER: 60/090252
PRIOR PILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090254
PRIOR APPLICATION NUMBER: 60/090355
PRIOR APPLICATION NUMBER: 60/090355
PRIOR APPLICATION NUMBER: 60/090429
PRIOR APPLICATION NUMBER: 60/090429
PRIOR APPLICATION NUMBER: 60/090439
PRIOR APPLICATION NUMBER: 60/090439
PRIOR APPLICATION NUMBER: 60/090431
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090540
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090659
PRIOR APPLICATION NUMBER:

APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-001

APPLICATION NUMBER: 60/ FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02

60/091544

FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091519

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US-09-312-283C-339
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                                                                                                                                                                                                                                         Patent No. 6534631 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID 0339
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                                                                                                                                                                                                                                                                              Sequence 118, Appl
Patent No. 6534631
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                               APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PC7/US99/15849
EARLIER FILING DATE: 1999-07-14
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APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated :
TITLE OF INVENTION: and Methods for Their
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
            EARLIER
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            APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIYPMEVLKTRMA--LRKTG---QYSGMLDCARRILAKEGVAAFYKGYIPNMLGIIPYAG
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Sleeman, Matthew
Onrust, Rene
                                                                                                                                                                                                                                                                                                       Application US/09482273
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         NUMBER:
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         60/092,921
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Pred. No. 1.7e-26;
2; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated from
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                                                                                                                                                                                                                                                                                                       US-09-501-558-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-501-558-2
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LENGTH: 335
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application Patent No. 6403784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/0 CURRENT FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 VISSTIANPTDVLKIRMQA----QGSLFQGSMIGS-FIDIYQQEGTRGLWRGVVPTAQRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 KDFLAGGIAAAISKTAVAPIERVKLLLQVQHAS-----KQIAADKQYKGIVDCIVRIPKE
                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FastSEQ
QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
                                                                                                                KDFLAGGIAAAISKTAVAPIERVKLLLQVQHAS-----KQIAADKQYKGIVDCIVRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNQRAIVGHVDLYKGTVDGILKMWKHEGFFALYKGFWPNWLRLGPWNIIFFITYEQLKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIYRAAYFGVYDTAK------GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGVLALYSGIAPALLRQASYGTIKIGIYQSLKRLFVERLEDET-----LLINMICGVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
                                                        KPFVYGGLASITAECGTFPIDLTKTRLQIQGQTNDAKFKEI----RYRGMLHALVRIGRE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATVVGVELPVYDITKKHLILSGMMGDTILTHFVSSF----TCGLAGALASNPVDVVRTRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mathur, Brian
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                                                                                                                                                                                                          Score 283.5; DB '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 286; DB 4;
Pred. No. 6.9e-24;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                      DB 4;
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Indels Length 291;

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Sequence 4. Application US/09160119A
Sequence 4. Application US/09160119A
PARENT NO. 6316219
GRMERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
STILE REFERENCE: GH-30985
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160/119A
CURRENT EFLING DATE: 1990-02-4
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: BP 98401655.0
SEAUTHER APPLICATION SAPIENS
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
SEAUTHER APPLICATION SAPIENS
US-09-160-119-4
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US-09-160-119-4
RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 MMQSG-RKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKK 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 IIYRAAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM 238
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                                                                                                                                                                                           320 LQVAARAGQTTYSGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYEL 374
                                                                                                                                                                                                                                                                                                                                                                                          181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAV-AGVVSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 YEGFFGLYRGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP-----LAAEILAG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 EGLKALYSGIAPAMLRQASYGTIKIGTYQSLKRLFIERPEDET----LPINVICGILSG 117
                                                                                                                                                                                                                                                                                                                              262 FLRDIPFSAIYFPCYAHVKASFANEDGOVSPGSLLLAGAIAGMPAASLVTPADVIKTR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 EQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL---GGYDKHTQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 QVAESAYRFGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 18.1%; Score 280; DB 4; Length 447; 1 Similarity 27.1%; Pred. No. 5.1e-23; 80; Conservative 47; Mismatches 148; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 QAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK 63
                                                                                                                                                                                                                                                              MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDEL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGGSQVIFTNPLEIVKIRLQV-AGEITTGPRVSAL----SVVRDLGFFGIYKGAKAC 261
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APPLICANT; KRIEF, STEPHANE
APPLICANT; SORCHET, MICHEL
APPLICANT; BRIL, ANTOINE
TITLE OF INVENTION: MOVEL COMPOUNDS
FILE REFERENCE: 6H-30085
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID MOS: 4
SOFTWARE: FBSTSEQ for Windows Version 3.0
SEQ ID MO 2
LENGTH: 674
TYPE: DET
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                                                                                                     ; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANIZM: HOMO SAPIEN
US-09-142-565-2
                                                                                                                                                                                                                                                                                            APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
APPLICANT: Robert James
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
CURRENT ELLING DATE: 199-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER APPLICATION NUMBER: 9705305.1
EARLIER APPLICATION NUMBER: 97050505.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-142-565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09142565A Patent No. 6187560 GENERAL INFORMATION:
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              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 GCAGGSQVIFTNPLEIVKIRLQV-AGEITTGPRVSAL-----SVVRDLGFFGIYKGAKAC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 YEGFFGLYRGLLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVP-----LAAEILAG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 QVAESAYRFGLGSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAV-AGVVSYPFDTVRRRMM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFL---GGVDKHTQFWRYFAGNLASG 120
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                  17.2%;
27.1%;
                  score 265; DB 3; Length 312;
Pred. No. 1.5e-21;
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US-08-518-878B-56
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                                                                                        US-08-518-878B-56
                                Matches
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                                                                                                                                                             TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 78: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/518,878B FILING DATE: 23-AUG-1995 CLASSIFICATION: 435
                                                                                                      TOPOLOGY: un
                                                                                                                                 TYPE:
                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
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                                                                                                                                             LENGTH:
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o. 5702902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 RYM-----NSPPGQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 MRNAIVNCAEVVTYDILKEKLLD---YHLLTDNFPCHFVSAFGAGFCATVVASPVDVVKT
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12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              10036-2711
                                             Similarity
                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
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                                                                                                                                               299 amino acids
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                                Conservative
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SYSTEM: PC-DOS/MS-DOS
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                            Score 250.5; DB 1;
Pred. No. 6e-20;
2; Mismatches 146;
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US-08-470-868A-56
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                                                                                                                                Matches
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                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                             Local
                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                           TELEFAX: (212
TELEX: 66441
                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                             Similarity
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                                                                                                                              Conservative
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                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                        (212) 790-9090
                                                                                                                                                                                                                                                                                           PENNIE
                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                         869-8864
                                                                                                                                          16.2%;
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Sequence 56, Application US/08470868A Patent No. 5861485
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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                                                                                                                                                                      12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL
SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV
                                                 SEWRGNLANVIRYEPTQALNEAFKDKYKQIFLGGVDKHTQEWRYFAGNLASGGAAGATSL
                                                                                                                 FLGAGTAACTADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/470,868A
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                                                                                                                                                                                                                                ; Score 250.5; DB; Pred. No. 6e-20; 52; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7853-0031-999
                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                   146;
                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                           299;
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RESULT 15
US-08-518-878B-51
(Sequence 51, Application US/08518878B
; Patent No. 5702902
; Patent NO. 1702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: COMPOSITIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: sindle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIDM TYPE: Floppy disk

MEDIDM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/518,878B

FILIMS DATE: 23-AUG-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: COTUZZI, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-036

TELEPHONE: (212) 790-990

TELEPHONE: (212) 790-990
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TATTAGIIA, LOUIS A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1155 Aver
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                      Match 16.2%; Score 250.5; DB 1; Length 309;
Local Similarity 24.9%; Pred. No. 6.3e-20;
les 74; Conservative 52; Mismatches 146; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GNGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM---- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 CFYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 -- NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 AAYFGYYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS 242
                                                                                                 132 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 190
                                                                                                                                                129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
191 CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM--- 243
                                                  189 AAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS 242
                                                                                                                                                                                                                                                                                                                                                      12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68
                                                                                                                                                                                                      77 SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV 131
                                                                                                                                                                                                                                                        69 SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                       17 FLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR 76
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Search completed: August 18, 2003, 16:15:11 Job time : 30 secs

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Minimum DB
Maximum DB
                                                                                                                                                                                                                                                         Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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        Pred. No. is the score greater than and is derived
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1385.5
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760.5
749.5
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734.5
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                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                                                                                                 is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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: //cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
: //cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
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   0 US-09-185-904A-32

US-09-811-094-31

0 US-09-810-644-31

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10 US-09-185-904A-31

10 US-09-185-904A-31

10 US-09-34-569-170

15 US-10-128-714-3338

15 US-10-128-714-3338

12 US-10-141-4714-338

12 US-10-259-165-192
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US-09-810-644-33
US-09-811-094A-3
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US-09-810-644-32
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Sequence 33, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 22, App
Sequence 338, Ap
Sequence 370, Appl
Sequence 370, Appl
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-666-	-09-997-	-09-993-667-	-653	-734-	-687	US-09-990-436-289	-09-989-730-	-181	-09-990	US-09-989-735-289	-09-989	-09-992	-09-989-721-	-456-	US-09-993-604-289	-09-991-163-	-09-990-442-	US-09-991-073-289	US-09-989-732-289	US-09-989-731-289	727-28	Ŋ	١.	722-28	-921A-	US-09-777-921A-2	S-09-777-9	-09-864-761-364	US-09-925-301-1459
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ALIGNMENTS

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APPLICANT: MOOS, Walter H.

APPLICANT: Pel, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT FILING DATE: 2001-03-14
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
CRGANISM: Homo sapien
US-09-811-094-33
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APPLICANT: Davis, Rot
APPLICANT: Clevenger,
APPLICANT: Wiley, San
APPLICANT: Willer, Sc
APPLICANT: Scabo, Tom
APPLICANT: Ghosh, Sou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                    Matches 298;
                                                                                                                                                     Query Match
Best Local :
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                                                                                     1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQVKGIVDCIVR
                                                                                                                                                  Similarity
                                                                   MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                   Willer, Scott W. Szabo, Tomas R. Ghosh, Soumitra S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiley, Sandra Eileen
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                                                                                                                                    100.0%;
illarity 100.0%;
Conservative 0
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                                                                                                                                    0;
                                                                                                                                  Score 1543; DB 9;
Pred. No. 6e-157;
Mismatches 0;
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                                                                                                                                                                 Length
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WESULT 2
US-09-810-644-33
US-09-810-644-33
Sequence 33, Application US/09810644
Patent No. US20020012992A1
PATENT INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapien US-09-810-644-33
                                                                                                                RESULT 3
US-09-185-904A-33
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APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiler, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
                   Sequence 33, Application US/09185904A Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088.42003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                           241 QSGRKGADIMYIGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                               181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                                                           181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240
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                                                                                                                                                                                                                  241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
Davis, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1543; DB 9; Length 298; ilarity 100.0%; Pred. No. 6e-157; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels 0;
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                                                                                                                                         Sequence 32, Application US/09811094

Patent No. US2001004414A1

GENERAL INFORMATION:

APPLICANY: Anderson, Christen M.

APPLICANY: Davis, Robert E.

APPLICANY: Miley, Sandra Eileen

APPLICANY: Willer, Scott W.

APPLICANY: Willer, Scott W.

APPLICANY: Ghosh, Sounitra S.

APPLICANY: Ghosh, Sounitra S.

APPLICANY: Pel, Yazhong

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),

TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088 420D4

CURRENT APPLICATION NUMBER: US/09/811,094

CURRENT APPLICATION NUMBER: US/09/811,094

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 37

SEC ID NO 32

LENGTH: 298

TYPE: PAT
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SEQ ID NO 3
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
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US-09-811-094-32
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Best Local S
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APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, Sandra Elleen
APPLICANT: Wiley, South W.
APPLICANT: Scabo, Tomas R.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Ghosh, Sounitra S.
APPLICANT: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088 420
CUGRENT APPLICATION NUMBER: US/09/185,904A
CUGRENT APPLICATION NUMBER: US/09/185,904A
CUGRENT FILLING DATE: 1998-11-03
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              Query Match
Best Local Similarity
                                                                                                       ORGANISM: Homo sapien
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              94.2%;
                Score 1454; DB 9;
Pred. No. 2e-147;
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Query Match Best Local S

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APPLICANT:

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RESULT 5
US-09-810-644-32
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; ORGANISM: Homo sapien
US-09-810-644-32
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Scabb, Tomas R.
APPLICANT: Ghosh, Soumitra S.
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CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEO ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
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No. US20020012992A1
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   QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                              GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS 180
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Pei, Yazhong
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92.6%;
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Pred. No. 2e-147;
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; ORGANISM: HOMO
US-09-185-904A-32
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US-09-185-904A-32
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SEQ ID NO 32
LENGTH: 298
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Best Local
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Patent No. US20020177185A1
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APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
                                            APPLICANT: MOOS, Walter H.
APPLICANT: Pe1, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.42004
                                                                                                                                                                                                      APPLICANT: Anderson, Christen M. APPLICANT: Davis, Robert E.
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
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Wiley, Sandra Eileen
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APPLICANT: Davis, Robert E.

APPLICANT: Davis, Robert E.

APPLICANT: Davis, Robert E.

APPLICANT: Wiley, Sandra Elleen

APPLICANT: Wiley, Sandra Elleen

APPLICANT: Wiley, Sandra Elleen

APPLICANT: Wiley, Sounttra S.

APPLICANT: Ghosh, Sounttra S.

APPLICANT: MOOS, Walter H.

APPLICANT: MOOS, WALTER AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088.420D3

CURRENT FILING DATE: 2001-03-14

CURRENT FILING DATE: 2001-03-14

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 31

LENGTH: 297

Type: PRT
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-31
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US-09-810-644-31
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-31
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Best Local S
Matches 260
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LENGTH: 297
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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121 GAAGATSLCFVYDLDFARTRLAADVGKSGTEREERGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                           260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IPKEQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
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                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                  89.8%; Score 1385.5; DB 9; Length 297;
87.2%; Pred. No. 4.4e-140;
ative 21; Mismatches 16; Indels 1;
                                                                                                                                                                                                                                          16; Indels 1;
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                                                                                                                                                                                                                                            Gaps
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Sequence 31, Application US/09185904A

Fatent No. US20020177185A1

GENERAL INFORMATION:

APPLICANT: DAYLS, Robert E.

APPLICANT: DAYLS, Robert E.

APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sounditra S.

APPLICANT: Goth, Sounditra S.

APPLICANT: Ghosh, Sounditra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION THEREFOR
TILE REFERENCE: 660088.420

CURRENT FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 33

SOPTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 31

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US-09-185-904A-31
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RESULT 10
US-09-801-368-252
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                                                                                            181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240
                                                                                                                                                                                                                                                                                                  121 GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS 179
                                                                                                                                                                                                                                                                                                                                             121 GAAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260;
                                                                                                                                                                                                                                                                                                                                                                                              61 IPKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR 60
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Similarity 87.2%; Pred. No. 4.4e-140;
60; Conservative 21; Mismatches 16; Indels 1; Gaps
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Sequence 252, Application US/09801368; Patent No. US20020128250Al GENERAL INFORMATION:
APPLICANT: Busby, Robert APPLICANT: Busby, Robert APPLICANT: Hecht, Peter APPLICANT: Hecht, Peter APPLICANT: Holtzman, Doug APPLICANT: Maxon, Mary

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APPLICANT: Lerchl, Jens
APPLICANT: Renz, Andreas
APPLICANT: Reinard, Thomas
APPLICANT: Reindl, Andreas
APPLICANT: Reindl, Andreas
APPLICANT: Reindl, Andreas
APPLICANT: Cirpus, Petra
APPLICANT: Cirpus, Petra
APPLICANT: Frank, Markus
APPLICANT: Frank, Markus
APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Reski, Ralf
APPLICANT: Reski, Ralf
TITLE OF INVENTION: in the synthesis of carbohydrates
TITLE OF INVENTION: in the synthesis of carbohydrates
FILE REFERENCE: BASF-NAE-1332-99-US
CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 1909-12-16
PRIOR APPLICATION NUMBER: US 60/171,101
PRIOR APPLICATION DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1
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US-09-734-569-170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
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Patent No. US20020064816A1
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LENGTH: 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Summers, Eric TITLE OF INVENTION: Methods for Improving FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 LSLLFVYSLDYARTRLAADSKSSKKGGARQFNGLIDVYKKTLKSDGVAGLYRGFLPSVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 TSLCFVYPLDFARTRLAAD--VGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 GVISFWRGNTANVIRYFPTQALNFAFKDKIKAMF - - GFKKEEGYAKWFAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 49.3%; Score 760.5; DB 10; Length Similarity 53.7%; Pred. No. 4.4e-73; 59; Conservative 42; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQA---VKYDGAFDCLRKIVAAEGVGSLFKGCGANILRGVAGAGVISMYDQLQMIL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salama, Sofie
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No. US20020128250Alman,
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                                                                                                                                                                           encoding proteins involved
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                                                                                                                                               ; ORGANISM: Aspergillus fumigatus US-10-128-714-3338
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US-10-128-714-3338
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APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PELICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR PELICATION NUMBER: US 60/316,362
PRIOR PELICATION NUMBER: US 60/316,362
PRIOR PELICATION NUMBER: US 60/316,362
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Best Local S
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LENGTH:
                                                                         Matches
                                                                                                                                                                                                                     SEQ ID NO 3338
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                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 8603 SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 SSLLFVYSLDYARTRLANDAKSSKKGGGERQFNGLVDVYKKTLATDGIAGLYRGFAISCA
                                                                       154;
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                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIIVYRGIYFGIYDSLKPVVLVGNLEGNFLASFLLGWGITIGAGLASYPIDTVRRMMMT
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                    SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAA---DKQYKGIVDCIVRIPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEMTDELMGGVSAAVSKTAAAPIERVKLLIQNQDEMLKSGRLSHPYKGIGECESRTVKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGEA---VKYNGSMDAFKQILAKEGAKSLFKGAGANILRAVAGAGVLSGYDQLQ 373
AFTDSFAVGGVSAAVSKTAAAPIERIKLL--VQNQDEMIRAGRLDRKYNGIIDCFRRTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                         Conservative
                                                                                      47.8%;
51.7%;
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                                                                     ; Pred.
47; Mis
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                                                                   Score 737; DB 15;
Pred. No. 1.4e-70;
7; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 749.5; DB 9
Pred. No. 8.6e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Essential Genes in Aspergillus fumigatus and
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                                                                                                         Length 308;
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                                                                     Gaps
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APPLICANT: Hu, Weingl
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Lemidux, Alexey M
APPLICANT: Lemidux, Sebastien M
ITILE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITILE OF INVENTION: Methods of Use
FILE REFERENCE: 10189-018-999
CURRENT EPILICATION UNMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-08-03
SOFTWARE: PRICATION NOS: 8603
SOFTWARE: PRICATION NOS: 8603
SOFTWARE: DRIEN 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PRICATION NOS: 8603
LEMCATH: 308
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US-10-128-714-8338
US-10-128-714-8338
; Sequence 8338, Application US/10128714
Publication No. US20030119013A1
; GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Aspergillus fumigatus US-10-128-714-8338
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182
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241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154;
                                                                                        184 LGIVVYRGLYFGMYDSIKPVVLVGSLEGSFLASFLLGWTVTTGAGIASYPLDTIRRRMMM 243
                                                                                                                                                   182 QGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                             124 GATSLLFVYSLDYARTRLANDAKSAKGGGERQFNGLIDVYRKTLASDGIAGLYRGFGPSV 183
                                                                                                                                                                                                                                                                        124 GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 181
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                                                                                                                                                                                                                                                                                                                                                                        64 EQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                          65 AEGVMSLWRGNTANVIRYFPTQALNFAFRDTYKSMFAYKKDR-DGYAKWMMGNLASGGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AFTDSFAVGGVSAAVSKTAAAPIERIKLL--VQNQDEMIRAGRLDRKYNGIIDCFRRTAQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAA----DKQYKGIVDCIVRIPK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.8%; Score 737; DB 15; Length 308; Similarity 51.7%; Pred. No. 1.4e-70; 54; Conservative 47; Mismatches 85; Indels 12;
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                             RESULT 15
US-10-259-165-192
; Sequence 192, Applicati
; Publication No. US20030
; GENERAL IMFORMATION;
; APPLICANT: Zhu, Tong
; APPLICANT: Chang, Nun
; APPLICANT: Briggs, St
; APPLICANT: Glazebrook
APPLICANT: Glazebrook
; APPLICANT: Katagiri,
; APPLICANT: Katagiri,
; APPLICANT: Katagiri,
; APPLICANT: Katagiri,
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US-10-141-478A-2
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CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: US 60/289,519
PRIOR APPLICATION NUMBER: US 60/289,519
PRIOR PRICHATION NUMBER: 60/289,527
PRIOR PRILICATION NUMBER: 60/289,527
PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 165
PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 165
PRIOR PRICHATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 165
PRIOR PRI DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 4
SOCTWARE: PATENTIAL VERSION 3.0
SEQ ID NO 2
LENGTH: 381
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 RRMMMTSNEA---VKYKSSLDAFKQILKNEGAKSLFKGAGANILRAVAGAGVLSGYDKLT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 RRMMMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 CYGIIYYRGLYFGLYDSYKPYLLTGDLQDSFFASFALGWYI----TNGAGLASYPIDTYR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VQGIIIYRAAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 GASSLLFVYSLDYARTRLANDAKAAKKGGGGRQFDGLVDVYRKTLKTDGIAGLYRGFNIS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GATSLCFVYPLDFARTRLAAD -- - VGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
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                             Wang, Xun
Chang, Hur-song
Chang, Hur-song
Briggs, Steven P.
Cooper, Bret
Glazebrook, Jane
Goff, Stephen A.
Katagiri, Fumiyaki
       Kreps, Joel
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o. US20030135888A1
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APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
ITILE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT PILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NO 19: 560/368,327
PRIOR FILING DATE: 2001-09-26
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 19: 782
LENGTH: 677
TYPE: PRI
COURSEMENT OF SERVICE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρy
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US-10-259-165-192
Search completed: August 18, 2003, 16:23:10 Job time : 59 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660
                                                                                                                                                                                                                                                                                                549 HLPVLVS--LSNRGLYFGMYDSLKPVVLVGNLQD----NFLASFLLGWGITIGAGLASYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 GFSVSVQGIIIYRAAYFGVYDTAK-----GMLDDPKNTHIVVSWMIAQTVTAVAGVVSYP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 YDELKKVI 298
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